

Panel 4D Summary: Ag3471 The CG59564-01 gene, a sorting nexin homolog, is most highly expressed in normal colon (CT=30). In addition, this gene is expressed at high to moderate levels in a wide range of cell types of significance in the immune response in health and disease. These cells include members of the T-cell, B-cell, endothelial cell, macrophage/monocyte, and peripheral blood mononuclear cell family, as well as epithelial and fibroblast cell types from lung and skin, and normal tissues represented by colon, lung, thymus and kidney. This ubiquitous pattern of expression suggests that this gene product may be involved in homeostatic processes for these and other cell types and tissues. This pattern is in agreement with the expression profile in General_screening_panel_v1.4 and also suggests a role for the gene product in cell survival and proliferation. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

AY. CG59553-01: Secretory protein SEC8

Expression of gene CG59553-01 was assessed using the primer-probe set Ag3465, described in Table AYA. Results of the RTQ-PCR runs are shown in Tables AYB, AYC and AYD.

Table AYA. Probe Name Ag3465

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-ttcacagcaagaagatgaacct-3'	22	616	547
Probe	TET-5'-tcatagatgaactacaccggcacctg-3'- TAMRA	26	649	548
Reverse	5'-ctcggctagtcgatttgatgt-3'	21	676	549

Table AYB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3465, Run 210376516	Tissue Name	Rel. Exp.(%) Ag3465, Run 210376516
AD 1 Hippo	21.3	Control (Path) 3 Temporal Ctx	8.2
AD 2 Hippo	33.0	Control (Path) 4 Temporal Ctx	40.9
AD 3 Hippo	11.0	AD 1 Occipital Ctx	20.7

AD 4 Hippo	11.6	AD 2 Occipital Ctx (Missing)	0.0
AD 5 Hippo	87.7	AD 3 Occipital Ctx	10.3
AD 6 Hippo	46.7	AD 4 Occipital Ctx	24.8
Control 2 Hippo	29.7	AD 5 Occipital Ctx	40.6
Control 4 Hippo	20.4	AD 6 Occipital Ctx	25.3
Control (Path) 3 Hippo	14.2	Control 1 Occipital Ctx	6.7
AD 1 Temporal Ctx	21.3	Control 2 Occipital Ctx	59.9
AD 2 Temporal Ctx	38.7	Control 3 Occipital Ctx	21.8
AD 3 Temporal Ctx	8.2	Control 4 Occipital Ctx	11.8
AD 4 Temporal Ctx	30.8	Control (Path) 1 Occipital Ctx	79.6
AD 5 Inf Temporal Ctx	100.0	Control (Path) 2 Occipital Ctx	18.8
AD 5 Sup Temporal Ctx	58.2	Control (Path) 3 Occipital Ctx	4.0
AD 6 Inf Temporal Ctx	47.6	Control (Path) 4 Occipital Ctx	25.7
AD 6 Sup Temporal Ctx	52.1	Control 1 Parietal Ctx	14.2
Control 1 Temporal Ctx	11.8	Control 2 Parietal Ctx	56.6
Control 2 Temporal Ctx	42.0	Control 3 Parietal Ctx	23.8
Control 3 Temporal Ctx	22.8	Control (Path) 1 Parietal Ctx	75.3
Control 3 Temporal Ctx	14.0	Control (Path) 2 Parietal Ctx	29.7
Control (Path) 1 Temporal Ctx	64.6	Control (Path) 3 Parietal Ctx	8.5
Control (Path) 2 Temporal Ctx	47.0	Control (Path) 4 Parietal Ctx	52.9

Table AYC. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3465, Run 217118990	Tissue Name	Rel. Exp.(%) Ag3465, Run 217118990
Adipose	13.1	Renal ca. TK-10	60.7
Melanoma* Hs688(A).T	22.5	Bladder	37.9
Melanoma*	30.1	Gastric ca. (liver met.)	42.9

Hs688(B).T		NCI-N87	
Melanoma* M14	54.7	Gastric ca. KATO III	48.0
Melanoma* LOXIMVI	15.5	Colon ca. SW-948	5.5
Melanoma* SK-MEL-5	42.0	Colon ca. SW480	57.4
Squamous cell carcinoma SCC-4	8.7	Colon ca.* (SW480 met) SW620	37.4
Testis Pool	12.8	Colon ca. HT29	25.0
Prostate ca.* (bone met) PC-3	63.7	Colon ca. HCT-116	28.3
Prostate Pool	13.0	Colon ca. CaCo-2	46.7
Placenta	7.1	Colon cancer tissue	26.4
Uterus Pool	12.0	Colon ca. SW1116	8.6
Ovarian ca. OVCAR-3	37.4	Colon ca. Colo-205	6.9
Ovarian ca. SK-OV-3	21.5	Colon ca. SW-48	7.5
Ovarian ca. OVCAR-4	26.1	Colon Pool	21.8
Ovarian ca. OVCAR-5	42.0	Small Intestine Pool	25.5
Ovarian ca. IGROV-1	23.5	Stomach Pool	15.4
Ovarian ca. OVCAR-8	24.7	Bone Marrow Pool	9.4
Ovary	14.0	Fetal Heart	6.9
Breast ca. MCF-7	38.4	Heart Pool	11.1
Breast ca. MDA-MB-231	49.0	Lymph Node Pool	23.8
Breast ca. BT 549	45.4	Fetal Skeletal Muscle	11.9
Breast ca. T47D	74.7	Skeletal Muscle Pool	26.2
Breast ca. MDA-N	20.4	Spleen Pool	39.2
Breast Pool	22.8	Thymus Pool	39.8
Trachea	15.4	CNS cancer (glio/astro) U87-MG	100.0
Lung	6.8	CNS cancer (glio/astro) U-118-MG	54.7
Fetal Lung	41.5	CNS cancer (neuro;met) SK-N-AS	50.0
Lung ca. NCI-N417	12.2	CNS cancer (astro) SF-539	19.3
Lung ca. LX-1	26.1	CNS cancer (astro) SNB-75	75.3

Lung ca. NCI-H146	12.6	CNS cancer (glio) SNB-19	23.8
Lung ca. SHP-77	33.9	CNS cancer (glio) SF- 295	95.3
Lung ca. A549	43.8	Brain (Amygdala) Pool	11.6
Lung ca. NCI-H526	7.6	Brain (cerebellum)	12.2
Lung ca. NCI-H23	78.5	Brain (fetal)	32.5
Lung ca. NCI-H460	25.0	Brain (Hippocampus) Pool	12.7
Lung ca. HOP-62	28.5	Cerebral Cortex Pool	15.8
Lung ca. NCI-H522	25.0	Brain (Substantia nigra) Pool	11.7
Liver	2.0	Brain (Thalamus) Pool	17.7
Fetal Liver	18.7	Brain (whole)	15.6
Liver ca. HepG2	15.5	Spinal Cord Pool	12.5
Kidney Pool	36.6	Adrenal Gland	17.7
Fetal Kidney	26.8	Pituitary gland Pool	6.0
Renal ca. 786-0	55.5	Salivary Gland	7.0
Renal ca. A498	19.8	Thyroid (female)	6.6
Renal ca. ACHN	31.0	Pancreatic ca. CAPAN2	40.3
Renal ca. UO-31	48.0	Pancreas Pool	28.7

Table AYD. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3465, Run 166417102	Tissue Name	Rel. Exp.(%) Ag3465, Run 166417102
Secondary Th1 act	22.1	HUVEC IL-1beta	14.6
Secondary Th2 act	33.9	HUVEC IFN gamma	17.8
Secondary Tr1 act	44.4	HUVEC TNF alpha + IFN gamma	10.6
Secondary Th1 rest	33.4	HUVEC TNF alpha + IL4	8.3
Secondary Th2 rest	25.0	HUVEC IL-11	8.2
Secondary Tr1 rest	29.7	Lung Microvascular EC none	12.3
Primary Th1 act	14.3	Lung Microvascular EC TNFalpha + IL-1beta	14.8
Primary Th2 act	41.2	Microvascular Dermal EC none	15.5
Primary Tr1 act	46.7	Microvascular Dermal EC TNFalpha + IL-1beta	14.7
Primary Th1 rest	88.9	Bronchial epithelium TNFalpha + IL1beta	15.5
Primary Th2 rest	39.2	Small airway epithelium	14.0

		none	
Primary Tr1 rest	31.0	Small airway epithelium TNFalpha + IL-1beta	65.5
CD45RA CD4 lymphocyte act	20.6	Coronary artery SMC rest	18.3
CD45RO CD4 lymphocyte act	29.9	Coronary artery SMC TNFalpha + IL-1beta	12.5
CD8 lymphocyte act	23.0	Astrocytes rest	28.7
Secondary CD8 lymphocyte rest	24.1	Astrocytes TNFalpha + IL-1beta	31.6
Secondary CD8 lymphocyte act	18.7	KU-812 (Basophil) rest	19.8
CD4 lymphocyte none	19.5	KU-812 (Basophil) PMA/ionomycin	42.6
2ry Th1/Th2/Tr1_anti- CD95 CH11	37.4	CCD1106 (Keratinocytes) none	21.8
LAK cells rest	17.1	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	100.0
LAK cells IL-2	35.8	Liver cirrhosis	16.5
LAK cells IL-2+IL-12	32.3	Lupus kidney	23.5
LAK cells IL-2+IFN gamma	38.4	NCI-H292 none	48.6
LAK cells IL-2+ IL-18	32.5	NCI-H292 IL-4	45.1
LAK cells PMA/ionomycin	12.0	NCI-H292 IL-9	49.7
NK Cells IL-2 rest	24.7	NCI-H292 IL-13	26.4
Two Way MLR 3 day	31.4	NCI-H292 IFN gamma	25.3
Two Way MLR 5 day	19.6	HPAEC none	17.9
Two Way MLR 7 day	14.9	HPAEC TNF alpha + IL-1 beta	20.2
PBMC rest	18.4	Lung fibroblast none	39.2
PBMC PWM	18.7	Lung fibroblast TNF alpha + IL-1 beta	32.8
PBMC PHA-L	10.2	Lung fibroblast IL-4	28.3
Ramos (B cell) none	61.6	Lung fibroblast IL-9	20.4
Ramos (B cell) ionomycin	46.7	Lung fibroblast IL-13	19.5
B lymphocytes PWM	28.1	Lung fibroblast IFN gamma	26.6
B lymphocytes CD40L and IL-4	44.8	Dermal fibroblast CCD1070 rest	26.8
EOL-1 dbcAMP	33.2	Dermal fibroblast CCD1070 TNF alpha	50.7
EOL-1 dbcAMP PMA/ionomycin	25.5	Dermal fibroblast CCD1070 IL-1 beta	18.4

Dendritic cells none	30.1	Dermal fibroblast IFN gamma	19.2
Dendritic cells LPS	19.1	Dermal fibroblast IL-4	34.6
Dendritic cells anti-CD40	33.7	IBD Colitis 2	9.0
Monocytes rest	25.0	IBD Crohn's	12.4
Monocytes LPS	16.3	Colon	56.3
Macrophages rest	44.4	Lung	16.4
Macrophages LPS	14.4	Thymus	49.3
HUVEC none	20.4	Kidney	52.1
HUVEC starved	37.1		

CNS_neurodegeneration_v1.0 Summary: Ag3465 This panel does not show differential expression of the CG59553-01 gene in Alzheimer's disease. However, this expression profile confirms the presence of this gene in the brain. Please see Panel 1.4 for discussion of utility of this gene in the central nervous system.

General_screening_panel_v1.4 Summary: Ag3465 Highest expression of the CG59553-01 gene is seen in a brain cancer cell line (CTs=24). Expression of this gene is ubiquitous throughout this panel, with significant levels of expression in clusters of cell lines derived from brain, renal, colon, lung, breast, ovarian, and melanoma cancers. These high levels of expression in all the samples on this panel suggest a role for this gene in cell growth and proliferation.

This molecule is also expressed at high levels in all regions of the CNS examined. Therefore, therapeutic modulation of the expression or function of this gene may be useful in the treatment of neurologic disorders, such as Alzheimer's disease, Parkinson's disease, schizophrenia, multiple sclerosis, stroke and epilepsy.

Among tissues with metabolic function, this gene is expressed at high to moderate levels in pituitary, adipose, adrenal gland, pancreas, thyroid, and adult and fetal skeletal muscle, heart, and liver. This widespread expression among these tissues suggests that this gene product may play a role in normal neuroendocrine and metabolic and that dysregulated expression of this gene may contribute to neuroendocrine disorders or metabolic diseases, such as obesity and diabetes.

Panel 4D Summary: Ag3465 The CG59553-01 gene is expressed at high to moderate levels in a wide range of cell types of significance in the immune response in health and disease.

These cells include members of the T-cell, B-cell, endothelial cell, macrophage/monocyte, and peripheral blood mononuclear cell family, as well as epithelial and fibroblast cell types from lung and skin, and normal tissues represented by colon, lung, thymus and kidney. This ubiquitous pattern of expression suggests that this gene product may be involved in homeostatic processes for these and other cell types and tissues. This pattern is in agreement with the expression profile in General_screening_panel_v1.5 and also suggests a role for the gene product in cell survival and proliferation. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

AZ. CG59435-01 and CG59435-02: Human Nedd1

Expression of gene CG59435-01 and CG59435-02 was assessed using the primer-probe set Ag3437, described in Table AZA. Results of the RTQ-PCR runs are shown in Tables AZB, AZC and AZD. Please note that CG59435-02 represents a full-length physical clone of the CG59435-01 gene, validating the prediction of the gene sequence.

Table AZA. Probe Name Ag3437

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-tggtgctgaaagtggaaatc-3'	20	1536	550
Probe	TET-5'-cctctccatcatctaaccaacaaga-3'- TAMRA	26	1562	551
Reverse	5'-tgggcttcaatttcattctct-3'	21	1611	552

Table AZB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3437, Run 210374394	Tissue Name	Rel. Exp.(%) Ag3437, Run 210374394
AD 1 Hippo	8.9	Control (Path) 3 Temporal Ctx	6.9
AD 2 Hippo	25.7	Control (Path) 4 Temporal Ctx	27.9
AD 3 Hippo	18.2	AD 1 Occipital Ctx	26.6
AD 4 Hippo	13.2	AD 2 Occipital Ctx (Missing)	0.0
AD 5 hippo	52.9	AD 3 Occipital Ctx	7.6

AD 6 Hippo	100.0	AD 4 Occipital Ctx	26.6
Control 2 Hippo	26.1	AD 5 Occipital Ctx	26.8
Control 4 Hippo	26.2	AD 6 Occipital Ctx	21.8
Control (Path) 3 Hippo	14.7	Control 1 Occipital Ctx	9.0
AD 1 Temporal Ctx	35.8	Control 2 Occipital Ctx	23.5
AD 2 Temporal Ctx	27.7	Control 3 Occipital Ctx	17.8
AD 3 Temporal Ctx	14.6	Control 4 Occipital Ctx	14.6
AD 4 Temporal Ctx	23.3	Control (Path) 1 Occipital Ctx	70.2
AD 5 Inf Temporal Ctx	65.5	Control (Path) 2 Occipital Ctx	12.9
AD 5 Sup Temporal Ctx	47.0	Control (Path) 3 Occipital Ctx	4.9
AD 6 Inf Temporal Ctx	78.5	Control (Path) 4 Occipital Ctx	22.2
AD 6 Sup Temporal Ctx	92.0	Control 1 Parietal Ctx	13.3
Control 1 Temporal Ctx	10.9	Control 2 Parietal Ctx	50.0
Control 2 Temporal Ctx	23.5	Control 3 Parietal Ctx	13.1
Control 3 Temporal Ctx	17.9	Control (Path) 1 Parietal Ctx	35.4
Control 4 Temporal Ctx	12.8	Control (Path) 2 Parietal Ctx	26.6
Control (Path) 1 Temporal Ctx	37.4	Control (Path) 3 Parietal Ctx	5.4
Control (Path) 2 Temporal Ctx	44.4	Control (Path) 4 Parietal Ctx	29.3

Table AZC. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag ³⁴³⁷ , Run 217066730	Tissue Name	Rel. Exp.(%) Ag ³⁴³⁷ , Run 217066730
Adipose	10.0	Renal ca. TK-10	24.0
Melanoma* Hs688(A).T	25.7	Bladder	18.6
Melanoma* Hs688(B).T	27.5	Gastric ca. (liver met.) NCI-N87	100.0
Melanoma* M14	34.9	Gastric ca. KATO III	60.3
Melanoma*	31.9	Colon ca. SW-948	9.7

LOXIMVI			
Melanoma* SK-MEL-5	8.7	Colon ca. SW480	61.6
Squamous cell carcinoma SCC-4	24.8	Colon ca.* (SW480 met) SW620	46.3
Testis Pool	25.9	Colon ca. HT29	22.7
Prostate ca.* (bone met) PC-3	84.1	Colon ca. HCT-116	72.2
Prostate Pool	12.3	Colon ca. CaCo-2	32.8
Placenta	0.3	Colon cancer tissue	38.2
Uterus Pool	11.4	Colon ca. SW1116	7.5
Ovarian ca. OVCAR-3	33.2	Colon ca. Colo-205	6.7
Ovarian ca. SK-OV-3	92.7	Colon ca. SW-48	7.1
Ovarian ca. OVCAR-4	9.7	Colon Pool	27.2
Ovarian ca. OVCAR-5	26.4	Small Intestine Pool	22.8
Ovarian ca. IGROV-1	16.5	Stomach Pool	12.3
Ovarian ca. OVCAR-8	6.5	Bone Marrow Pool	13.5
Ovary	7.6	Fetal Heart	21.9
Breast ca. MCF-7	24.3	Heart Pool	11.7
Breast ca. MDA-MB-231	84.1	Lymph Node Pool	30.4
Breast ca. BT 549	68.3	Fetal Skeletal Muscle	15.2
Breast ca. T47D	52.1	Skeletal Muscle Pool	28.5
Breast ca. MDA-N	18.9	Spleen Pool	15.8
Breast Pool	26.6	Thymus Pool	21.2
Trachea	9.2	CNS cancer (glio/astro) U87-MG	14.0
Lung	4.9	CNS cancer (glio/astro) U-118-MG	91.4
Fetal Lung	49.0	CNS cancer (neuro;met) SK-N-AS	55.5
Lung ca. NCI-N417	4.9	CNS cancer (astro) SF-539	14.5
Lung ca. LX-1	37.4	CNS cancer (astro) SNB-75	33.0
Lung ca. NCI-H146	6.8	CNS cancer (glio) SNB-19	12.5
Lung ca. SHP-77	51.4	CNS cancer (glio) SF-295	51.4

Lung ca. A549	33.9	Brain (Amygdala) Pool	0.0
Lung ca. NCI-H526	8.4	Brain (cerebellum)	1.5
Lung ca. NCI-H23	34.4	Brain (fetal)	6.2
Lung ca. NCI-H460	98.6	Brain (Hippocampus) Pool	3.0
Lung ca. HOP-62	15.2	Cerebral Cortex Pool	3.0
Lung ca. NCI-H522	37.9	Brain (Substantia nigra) Pool	3.6
Liver	0.4	Brain (Thalamus) Pool	3.9
Fetal Liver	26.8	Brain (whole)	1.1
Liver ca. HepG2	11.3	Spinal Cord Pool	5.0
Kidney Pool	23.2	Adrenal Gland	3.3
Fetal Kidney	42.9	Pituitary gland Pool	4.5
Renal ca. 786-0	41.5	Salivary Gland	0.9
Renal ca. A498	12.9	Thyroid (female)	4.2
Renal ca. ACHN	20.2	Pancreatic ca. CAPAN2	20.7
Renal ca. UO-31	29.7	Pancreas Pool	19.8

Table AZD. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag3437, Run 169839068	Tissue Name	Rel. Exp.(%) Ag3437, Run 169839068
Secondary Th1 act	44.8	HUVEC IL-1beta	23.2
Secondary Th2 act	57.8	HUVEC IFN gamma	26.2
Secondary Tr1 act	60.7	HUVEC TNF alpha + IFN gamma	18.6
Secondary Th1 rest	10.2	HUVEC TNF alpha + IL4	16.7
Secondary Th2 rest	14.3	HUVEC IL-11	10.9
Secondary Tr1 rest	13.9	Lung Microvascular EC none	28.1
Primary Th1 act	37.4	Lung Microvascular EC TNFalpha + IL-1beta	25.3
Primary Th2 act	34.9	Microvascular Dermal EC none	19.9
Primary Tr1 act	39.0	Microvascular Dermal EC TNFalpha + IL-1beta	17.3
Primary Th1 rest	17.8	Bronchial epithelium TNFalpha + IL1beta	20.9
Primary Th2 rest	14.7	Small airway epithelium none	4.9
Primary Tr1 rest	23.2	Small airway epithelium TNFalpha + IL-1beta	20.4
CD45RA CD4	39.0	Coronary artery SMC rest	10.7

lymphocyte act			
CD45RO CD4 lymphocyte act	37.4	Coronary artery SMC TNFalpha + IL-1beta	10.7
CD8 lymphocyte act	31.9	Astrocytes rest	9.2
Secondary CD8 lymphocyte rest	33.7	Astrocytes TNFalpha + IL-1beta	6.4
Secondary CD8 lymphocyte act	21.8	KU-812 (Basophil) rest	36.6
CD4 lymphocyte none	10.4	KU-812 (Basophil) PMA/ionomycin	100.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	15.7	CCD1106 (Keratinocytes) none	21.9
LAK cells rest	21.8	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	29.9
LAK cells IL-2	24.1	Liver cirrhosis	6.0
LAK cells IL-2+IL-12	33.2	NCI-H292 none	13.0
LAK cells IL-2+IFN gamma	38.4	NCI-H292 IL-4	25.2
LAK cells IL-2+ IL-18	33.9	NCI-H292 IL-9	32.8
LAK cells PMA/ionomycin	9.3	NCI-H292 IL-13	26.2
NK Cells IL-2 rest	27.9	NCI-H292 IFN gamma	37.9
Two Way MLR 3 day	23.2	HPAEC none	13.7
Two Way MLR 5 day	25.3	HPAEC TNF alpha + IL-1 beta	30.8
Two Way MLR 7 day	23.8	Lung fibroblast none	12.1
PBMC rest	9.1	Lung fibroblast TNF alpha + IL-1 beta	9.5
PBMC PWM	25.9	Lung fibroblast IL-4	11.7
PBMC PHA-L	27.7	Lung fibroblast IL-9	19.3
Ramos (B cell) none	23.5	Lung fibroblast IL-13	11.2
Ramos (B cell) ionomycin	23.0	Lung fibroblast IFN gamma	19.5
B lymphocytes PWM	36.3	Dermal fibroblast CCD1070 rest	66.9
B lymphocytes CD40L and IL-4	21.5	Dermal fibroblast CCD1070 TNF alpha	70.2
EOL-1 dbcAMP	21.0	Dermal fibroblast CCD1070 IL-1 beta	46.3
EOL-1 dbcAMP PMA/ionomycin	19.8	Dermal fibroblast IFN gamma	17.1
Dendritic cells none	10.2	Dermal fibroblast IL-4	21.5
Dendritic cells LPS	10.8	Dermal Fibroblasts rest	8.9
Dendritic cells anti-	9.1	Neutrophils TNFa+LPS	0.5

CD40			
Monocytes rest	10.1	Neutrophils rest	5.7
Monocytes LPS	11.6	Colon	5.5
Macrophages rest	13.9	Lung	10.7
Macrophages LPS	15.7	Thymus	39.2
HUVEC none	11.8	Kidney	8.8
HUVEC starved	18.7		

CNS_neurodegeneration_v1.0 Summary: Ag3437 This panel confirms the expression of CG59435-01 gene at low levels in the brains of an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. Please see Panel 1.4 for a discussion of the potential utility of this gene in treatment of central nervous system disorders.

General_screening_panel_v1.4 Summary: Ag3437 The CG59435-01 is gene is ubiquitously expressed in this panel, with highest expression in a gastric cancer cell line (CT=26.5). In addition, significant levels of expression are evident in cell lines from brain cancer, colon cancer, ovarian cancer, breast cancer, prostate cancer and lung cancer. Thus, expression of this gene could be used as a marker to detect the presence of these cancers. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of these cancers.

In addition, this gene is expressed at moderate to low levels in pituitary, adipose, adrenal gland, pancreas, thyroid, and adult and fetal skeletal muscle, heart, and liver. This widespread expression among metabolic tissues suggests that this gene product may play a role in normal neuroendocrine and metabolic and that dysregulated expression of this gene may contribute to neuroendocrine disorders or metabolic diseases, such as obesity and diabetes.

In addition, the CG59435-01 gene encodes a homologue of mouse NEDD1 protein. Nedd is an acronym of "neural precursor cell expressed developmentally and down-regulated" (Ref 1) The developmentally regulated mouse gene Nedd1 encodes a protein with similarities to the beta subunit of heterotrimeric GTP-binding proteins that has growth suppressing activity when overexpressed in various cultured cell types. Nedd1 mRNA is shown to be strongly expressed in early embryonic brain and may play a role in the differentiation-coupled growth arrest in neuronal cells (Ref. 2). The moderate to low levels (CT=30-33) in all regions of the central nervous system examined suggest that this gene product may also play a role in the

differentiation-coupled growth arrest in neuronal cells. Furthermore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

References:

1. Kumar S, Tomooka Y, Noda M. (1992) Identification of a set of genes with developmentally down-regulated expression in the mouse brain. *Biochem Biophys Res Commun* 185(3):1155-61
2. Kumar S, Matsuzaki T, Yoshida Y, Noda M. (1994) Molecular cloning and biological activity of a novel developmentally regulated gene encoding a protein with beta-transducin-like structure. *J Biol Chem* 269(15):11318-26.

Panel 4.1D Summary: Ag3437 The CG59435-01 is gene is ubiquitously expressed in this panel, with highest expression in the basophil cell line KU-812 treated with PMA/ionomycin (CT=27.9). This gene is expressed at high to moderate levels in a wide range of cell types of significance in the immune response in health and disease. These cells include members of the T-cell, B-cell, endothelial cell, macrophage/monocyte, and peripheral blood mononuclear cell family, as well as epithelial and fibroblast cell types from lung and skin, and normal tissues represented by colon, lung, thymus and kidney. This ubiquitous pattern of expression suggests that this gene product may be involved in homeostatic processes for these and other cell types and tissues. This pattern is in agreement with the expression profile in *General_screening_panel_v1.4* and also suggests a role for the gene product in cell survival and proliferation. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

BA. CG59439-01 and CG59439-02: Xenobiotic/medium-chain fatty acid:CoA ligase form XL-III

Expression of gene CG59439-01 was assessed using the primer-probe set Ag3438, described in Table BAA. Results of the RTQ-PCR runs are shown in Table BAB. Please note that CG59439-02 represents a full-length physical clone of the CG59439-01 gene, validating the prediction of the gene sequence.

Table BAA. Probe Name Ag3438

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-accccathtaaccacttttgg-3'	20	938	553
Probe	TET-5'-tcatttatatatcgatgattctgcagca-3'-TAMRA	29	964	554
Reverse	5'-gaacctgatgctggtgaaatc-3'	21	994	555

Table BAB. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag3438, Run 198383568	Tissue Name	Rel. Exp.(%) Ag3438, Run 198383568
Secondary Th1 act	4.0	HUVEC IL-1beta	0.0
Secondary Th2 act	100.0	HUVEC IFN gamma	0.0
Secondary Tr1 act	25.9	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	0.0	HUVEC IL-11	0.0
Secondary Tr1 rest	0.0	Lung Microvascular EC none	0.0
Primary Th1 act	0.0	Lung Microvascular EC TNFalpha + IL-1beta	0.0
Primary Th2 act	0.0	Microvascular Dermal EC none	0.0
Primary Tr1 act	0.0	Microvascular Dermal EC TNFalpha + IL-1beta	0.0
Primary Th1 rest	0.0	Bronchial epithelium TNFalpha + IL1beta	9.4
Primary Th2 rest	0.0	Small airway epithelium none	7.0
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	13.8
CD45RA CD4 lymphocyte act	16.3	Coronary artery SMC rest	0.0
CD45RO CD4 lymphocyte act	0.0	Coronary artery SMC TNFalpha + IL-1beta	0.0

CD8 lymphocyte act	0.0	Astrocytes rest	0.0
Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFalpha + IL-1beta	0.0
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	25.9
CD4 lymphocyte none	12.9	KU-812 (Basophil) PMA/ionomycin	10.5
2ry Th1/Th2/Tr1 _anti-CD95 CH11	0.0	CCD1106 (Keratinocytes) none	0.0
LAK cells rest	6.9	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0
LAK cells IL-2	6.1	Liver cirrhosis	20.4
LAK cells IL-2+IL-12	7.7	NCI-H292 none	0.0
LAK cells IL-2+IFN gamma	13.6	NCI-H292 IL-4	6.7
LAK cells IL-2+ IL-18	14.2	NCI-H292 IL-9	11.7
LAK cells PMA/ionomycin	0.0	NCI-H292 IL-13	25.9
NK Cells IL-2 rest	0.0	NCI-H292 IFN gamma	17.2
Two Way MLR 3 day	14.9	HPAEC none	0.0
Two Way MLR 5 day	0.0	HPAEC TNF alpha + IL-1 beta	0.0
Two Way MLR 7 day	0.0	Lung fibroblast none	0.0
PBMC rest	4.4	Lung fibroblast TNF alpha + IL-1 beta	0.0
PBMC PWM	2.7	Lung fibroblast IL-4	0.0
PBMC PHA-L	21.2	Lung fibroblast IL-9	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-13	0.0
Ramos (B cell) ionomycin	0.0	Lung fibroblast IFN gamma	0.0
B lymphocytes PWM	0.0	Dermal fibroblast CCD1070 rest	0.0
B lymphocytes CD40L and IL-4	11.1	Dermal fibroblast CCD1070 TNF alpha	0.0
EOL-1 dbcAMP	12.2	Dermal fibroblast CCD1070 IL-1 beta	0.0
EOL-1 dbcAMP PMA/ionomycin	0.0	Dermal fibroblast IFN gamma	0.0
Dendritic cells none	6.9	Dermal fibroblast IL-4	0.0
Dendritic cells LPS	0.0	Dermal Fibroblasts rest	0.0
Dendritic cells anti-CD40	0.0	Neutrophils TNFa+LPS	0.0
Monocytes rest	6.4	Neutrophils rest	4.8
Monocytes LPS	0.0	Colon	5.5

Macrophages rest	7.0	Lung	0.0
Macrophages LPS	0.0	Thymus	3.6
HUVEC none	0.0	Kidney	22.4
HUVEC starved	0.0		

CNS_neurodegeneration_v1.0 Summary: Ag3438 Expression of the CG59439-02 gene is low/undetectable in all samples on this panel (CTs>35). (Data not shown.)

General_screening_panel_v1.4 Summary: Ag3438 Results from one experiment with the CG59439-02 gene are not included. The amp plot indicates that there were experimental difficulties with this run.

Panel 4.1D Summary: Ag3438 Expression of the CG59439-02 gene is restricted to a sample derived from chronically activated Th2 cells (CT=33).

Panel 4D Summary: Ag3438 Results from one experiment with the CG59439-02 gene are not included. The amp plot indicates that there were experimental difficulties with this run.

BB. CG59354-01 and CG59354-02 and CG59354-03: phosducin-like protein

Expression of gene CG59354-01 and variant CG59354-02 was assessed using the primer-probe set Ag3553, described in Table BBA. Results of the RTQ-PCR runs are shown in Tables BBB, BBC and BBD. Please note that CG59354-03 represents a full-length physical clone of the CG59354-01 gene, validating the prediction of the gene sequence.

Table BBA. Probe Name Ag3553

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-tctatttcaggtcgctatcct-3'	22	1778	556
Probe	TET-5'-acgcacagatgtcagaccaagactt-3'- TAMRA	26	1822	557
Reverse	5'-ggaatttggtactcccagaa-3'	22	1852	558

Table BBB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3553, Run 210641082	Tissue Name	Rel. Exp.(%) Ag3553, Run 210641082
AD 1 Hippo	11.3	Control (Path) 3 Temporal Ctx	3.7
AD 2 Hippo	17.8	Control (Path) 4 Temporal Ctx	19.6

AD 3 Hippo	4.8	AD 1 Occipital Ctx	15.6
AD 4 Hippo	4.6	AD 2 Occipital Ctx (Missing)	0.0
AD 5 hippo	70.2	AD 3 Occipital Ctx	4.5
AD 6 Hippo	55.5	AD 4 Occipital Ctx	12.5
Control 2 Hippo	20.3	AD 5 Occipital Ctx	28.7
Control 4 Hippo	14.5	AD 6 Occipital Ctx	32.1
Control (Path) 3 Hippo	7.0	Control 1 Occipital Ctx	3.5
AD 1 Temporal Ctx	15.1	Control 2 Occipital Ctx	51.1
AD 2 Temporal Ctx	18.8	Control 3 Occipital Ctx	14.4
AD 3 Temporal Ctx	3.4	Control 4 Occipital Ctx	4.7
AD 4 Temporal Ctx	11.7	Control (Path) 1 Occipital Ctx	64.6
AD 5 Inf Temporal Ctx	100.0	Control (Path) 2 Occipital Ctx	8.0
AD 5 Sup Temporal Ctx	50.7	Control (Path) 3 Occipital Ctx	3.9
AD 6 Inf Temporal Ctx	69.7	Control (Path) 4 Occipital Ctx	11.8
AD 6 Sup Temporal Ctx	66.9	Control 1 Parietal Ctx	7.0
Control 1 Temporal Ctx	4.8	Control 2 Parietal Ctx	41.2
Control 2 Temporal Ctx	26.6	Control 3 Parietal Ctx	12.0
Control 3 Temporal Ctx	9.1	Control (Path) 1 Parietal Ctx	62.0
Control 4 Temporal Ctx	7.5	Control (Path) 2 Parietal Ctx	21.6
Control (Path) 1 Temporal Ctx	44.8	Control (Path) 3 Parietal Ctx	3.5
Control (Path) 2 Temporal Ctx	24.8	Control (Path) 4 Parietal Ctx	41.8

Table BBC. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3553, Run 217049381	Tissue Name	Rel. Exp.(%) Ag3553, Run 217049381
Adipose	5.2	Renal ca. TK-10	40.6
Melanoma* Hs688(A).T	40.3	Bladder	29.9

Melanoma* Hs688(B).T	31.9	Gastric ca. (liver met.) NCI-N87	39.5
Melanoma* M14	41.5	Gastric ca. KATO III	55.9
Melanoma* LOXIMVI	37.1	Colon ca. SW-948	9.0
Melanoma* SK- MEL-5	25.9	Colon ca. SW480	68.3
Squamous cell carcinoma SCC-4	17.9	Colon ca.* (SW480 met) SW620	23.5
Testis Pool	5.4	Colon ca. HT29	20.0
Prostate ca.* (bone met) PC-3	31.4	Colon ca. HCT-116	66.0
Prostate Pool	9.0	Colon ca. CaCo-2	32.8
Placenta	4.0	Colon cancer tissue	17.4
Uterus Pool	5.5	Colon ca. SW1116	4.0
Ovarian ca. OVCAR-3	40.1	Colon ca. Colo-205	11.3
Ovarian ca. SK-OV- 3	47.3	Colon ca. SW-48	9.9
Ovarian ca. OVCAR-4	11.4	Colon Pool	18.4
Ovarian ca. OVCAR-5	37.9	Small Intestine Pool	11.7
Ovarian ca. IGROV- 1	25.0	Stomach Pool	14.9
Ovarian ca. OVCAR-8	16.6	Bone Marrow Pool	6.9
Ovary	10.2	Fetal Heart	4.6
Breast ca. MCF-7	42.6	Heart Pool	6.6
Breast ca. MDA- MB-231	50.7	Lymph Node Pool	21.3
Breast ca. BT 549	81.8	Fetal Skeletal Muscle	3.8
Breast ca. T47D	85.9	Skeletal Muscle Pool	6.0
Breast ca. MDA-N	33.0	Spleen Pool	13.9
Breast Pool	17.3	Thymus Pool	11.1
Trachea	16.4	CNS cancer (glio/astro) U87-MG	44.4
Lung	5.3	CNS cancer (glio/astro) U-118-MG	45.4
Fetal Lung	33.7	CNS cancer (neuro;met) SK-N-AS	44.8
Lung ca. NCI-N417	5.8	CNS cancer (astro) SF- 539	31.0
Lung ca. LX-1	22.7	CNS cancer (astro) SNB-75	100.0

Lung ca. NCI-H146	16.7	CNS cancer (glio) SNB-19	27.4
Lung ca. SHP-77	59.5	CNS cancer (glio) SF- 295	59.5
Lung ca. A549	41.5	Brain (Amygdala) Pool	8.3
Lung ca. NCI-H526	5.4	Brain (cerebellum)	8.0
Lung ca. NCI-H23	31.0	Brain (fetal)	23.8
Lung ca. NCI-H460	33.4	Brain (Hippocampus) Pool	10.7
Lung ca. HOP-62	21.9	Cerebral Cortex Pool	15.1
Lung ca. NCI-H522	17.8	Brain (Substantia nigra) Pool	11.0
Liver	0.5	Brain (Thalamus) Pool	16.6
Fetal Liver	18.3	Brain (whole)	11.8
Liver ca. HepG2	9.2	Spinal Cord Pool	11.7
Kidney Pool	29.5	Adrenal Gland	6.5
Fetal Kidney	16.2	Pituitary gland Pool	4.7
Renal ca. 786-0	57.0	Salivary Gland	9.2
Renal ca. A498	7.9	Thyroid (female)	8.3
Renal ca. ACHN	20.9	Pancreatic ca. CAPAN2	30.4
Renal ca. UO-31	29.1	Pancreas Pool	21.3

Table BBD. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3553, Run 166487505	Tissue Name	Rel. Exp.(%) Ag3553, Run 166487505
Secondary Th1 act	45.4	HUVEC IL-1beta	17.0
Secondary Th2 act	42.9	HUVEC IFN gamma	39.2
Secondary Tr1 act	58.6	HUVEC TNF alpha + IFN gamma	27.4
Secondary Th1 rest	6.7	HUVEC TNF alpha + IL4	31.4
Secondary Th2 rest	14.5	HUVEC IL-11	23.7
Secondary Tr1 rest	15.0	Lung Microvascular EC none	41.2
Primary Th1 act	38.4	Lung Microvascular EC TNFalpha + IL-1beta	28.3
Primary Th2 act	24.5	Microvascular Dermal EC none	59.0
Primary Tr1 act	32.8	Microvascular Dermal EC TNFalpha + IL-1beta	23.5
Primary Th1 rest	57.0	Bronchial epithelium TNFalpha + IL1beta	21.5
Primary Th2 rest	43.2	Small airway epithelium	5.8

		none	
Primary Tr1 rest	39.0	Small airway epithelium TNFalpha + IL-1beta	52.5
CD45RA CD4 lymphocyte act	25.5	Coronary artery SMC rest	14.3
CD45RO CD4 lymphocyte act	34.6	Coronary artery SMC TNFalpha + IL-1beta	12.0
CD8 lymphocyte act	28.1	Astrocytes rest	18.2
Secondary CD8 lymphocyte rest	30.8	Astrocytes TNFalpha + IL-1beta	11.3
Secondary CD8 lymphocyte act	21.9	KU-812 (Basophil) rest	19.6
CD4 lymphocyte none	6.0	KU-812 (Basophil) PMA/ionomycin	71.2
2ry Th1/Th2/Tr1_anti- CD95 CH11	21.9	CCD1106 (Keratinocytes) none	31.6
LAK cells rest	24.8	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	9.0
LAK cells IL-2	32.8	Liver cirrhosis	4.1
LAK cells IL-2+IL-12	24.0	Lupus kidney	4.0
LAK cells IL-2+IFN gamma	37.6	NCI-H292 none	35.1
LAK cells IL-2+ IL-18	27.2	NCI-H292 IL-4	39.2
LAK cells PMA/ionomycin	16.8	NCI-H292 IL-9	49.0
NK Cells IL-2 rest	23.5	NCI-H292 IL-13	28.7
Two Way MLR 3 day	21.5	NCI-H292 IFN gamma	29.5
Two Way MLR 5 day	16.3	HPAEC none	38.2
Two Way MLR 7 day	17.6	HPAEC TNF alpha + IL-1 beta	27.2
PBMC rest	8.0	Lung fibroblast none	9.4
PBMC PWM	91.4	Lung fibroblast TNF alpha + IL-1 beta	11.1
PBMC PHA-L	33.9	Lung fibroblast IL-4	34.6
Ramos (B cell) none	29.5	Lung fibroblast IL-9	21.3
Ramos (B cell) ionomycin	85.3	Lung fibroblast IL-13	15.8
B lymphocytes PWM	100.0	Lung fibroblast IFN gamma	39.2
B lymphocytes CD40L and IL-4	33.0	Dermal fibroblast CCD1070 rest	45.1
EOL-1 dbcAMP	35.8	Dermal fibroblast CCD1070 TNF alpha	75.3
EOL-1 dbcAMP PMA/ionomycin	46.7	Dermal fibroblast CCD1070 IL-1 beta	37.4

Dendritic cells none	14.3	Dermal fibroblast IFN gamma	15.7
Dendritic cells LPS	15.2	Dermal fibroblast IL-4	25.9
Dendritic cells anti-CD40	22.2	IBD Colitis 2	1.4
Monocytes rest	10.4	IBD Crohn's	1.5
Monocytes LPS	16.7	Colon	16.7
Macrophages rest	27.9	Lung	12.2
Macrophages LPS	5.7	Thymus	28.7
HUVEC none	29.5	Kidney	28.5
HUVEC starved	67.4		

CNS_neurodegeneration_v1.0 Summary: Ag3553 This panel confirms the expression of CG59354-03 gene at low levels in the brains of an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. Please see Panel 1.4 for a discussion of the potential utility of this gene in treatment of central nervous system disorders.

General_screening_panel_v1.4 Summary: Ag3553 The CG59354-03 gene is ubiquitously expressed in this panel, with highest expression in a brain cancer cell line (CT=25.9). In addition, significant levels of expression are seen in cell lines derived from colon, breast, ovarian, renal, lung, prostate, and melanoma cancers. Furthermore, higher levels of expression are seen in fetal liver and lung (CTs=27-28) when compared to expression in the adult tissues (CTs=30-33). The high levels of expression in fetal tissue and cancer cell lines, both of which are highly proliferative, suggests that this gene product may be involved in cell growth and differentiation. Therefore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of cancer.

Among tissues with metabolic or endocrine function, this gene is expressed at high to moderate levels in pancreas, adipose, adrenal gland, thyroid, pituitary gland, skeletal muscle, heart, liver and the gastrointestinal tract. Therefore, therapeutic modulation of the activity of this gene may prove useful in the treatment of endocrine/metabolically related diseases, such as obesity and diabetes.

In addition, this gene is expressed at high levels in all regions of the central nervous system examined, including amygdala, hippocampus, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord. The CG59354-03 gene encodes a splice variant of

phosphoducin-like protein (PHLP). PDCL is a putative modulator of heterotrimeric G proteins. It was initially isolated as the product of an ethanol-responsive gene in neural cell cultures (Ref. 1). PDCL shares extensive amino acid sequence homology with phosducin (PDC), a phosphoprotein expressed in retina and pineal gland that inhibits several G protein-coupled signaling pathways by binding to the beta-gamma subunits of G proteins. Therefore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

References:

1. Miles MF, Barhite S, Sganga M, Elliott M. (1993) Phosducin-like protein: an ethanol-responsive potential modulator of guanine nucleotide-binding protein function. *Proc Natl Acad Sci U S A* 90(22):10831-5

Panel 4D Summary: Ag3553 The CG59354-03 gene is ubiquitously expressed in this panel, with highest expression in B cells treated with polk-weed mitogen (CT=27.2). In addition, this gene is expressed at high to moderate levels in a wide range of cell types of significance in the immune response in health and disease. These cells include members of the T-cell, B-cell, endothelial cell, macrophage/monocyte, and peripheral blood mononuclear cell family, as well as epithelial and fibroblast cell types from lung and skin, and normal tissues represented by colon, lung, thymus and kidney. This ubiquitous pattern of expression suggests that this gene product may be involved in homeostatic processes for these and other cell types and tissues. This pattern is in agreement with the expression profile in General_screening_panel_v1.4 and also suggests a role for the gene product in cell survival and proliferation. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

BC. CG59319-01 and CG59319-02: phosducin-like protein

Expression of gene CG59319-01 was assessed using the primer-probe set Ag3544, described in Table BCA. Results of the RTQ-PCR runs are shown in Tables BCB and BCC. Please note that CG59319-02 represents a full-length physical clone of the CG59319-01 gene, validating the prediction of the gene sequence.

Table BCA. Probe Name Ag3544

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-tacagatcaagcatcccaatgt-3'	22	347	559
Probe	TET-5'- tggttaaccagcatcttagtcttctagca-3'- TAMRA	29	375	560
Reverse	5'-ttcacgatggctttaacaaatt-3'	22	423	561

Table BCB. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3544, Run 217048127	Tissue Name	Rel. Exp.(%) Ag3544, Run 217048127
Adipose	0.0	Renal ca. TK-10	0.0
Melanoma* Hs688(A).T	0.0	Bladder	0.0
Melanoma* Hs688(B).T	0.0	Gastric ca. (liver met.) NCI-N87	0.7
Melanoma* M14	0.0	Gastric ca. KATO III	0.0
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.2
Melanoma* SK- MEL-5	0.0	Colon ca. SW480	0.0
Squamous cell carcinoma SCC-4	1.4	Colon ca.* (SW480 met) SW620	0.0
Testis Pool	100.0	Colon ca. HT29	0.0
Prostate ca.* (bone met) PC-3	0.0	Colon ca. HCT-116	0.3
Prostate Pool	0.0	Colon ca. CaCo-2	0.0
Placenta	0.0	Colon cancer tissue	0.0
Uterus Pool	0.0	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	1.2	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV- 3	0.9	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	0.0	Colon Pool	0.0
Ovarian ca. OVCAR-5	0.0	Small Intestine Pool	0.0
Ovarian ca. IGROV- 1	0.2	Stomach Pool	0.0
Ovarian ca. OVCAR-8	0.0	Bone Marrow Pool	0.0
Ovary	0.0	Fetal Heart	0.0

Breast ca. MCF-7	0.0	Heart Pool	0.0
Breast ca. MDA-MB-231	0.2	Lymph Node Pool	0.0
Breast ca. BT 549	0.0	Fetal Skeletal Muscle	0.0
Breast ca. T47D	0.3	Skeletal Muscle Pool	0.0
Breast ca. MDA-N	0.0	Spleen Pool	0.0
Breast Pool	0.0	Thymus Pool	0.0
Trachea	0.5	CNS cancer (glio/astro) U87-MG	0.0
Lung	0.0	CNS cancer (glio/astro) U-118-MG	0.0
Fetal Lung	0.0	CNS cancer (neuro;met) SK-N-AS	0.0
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF-539	0.3
Lung ca. LX-1	0.0	CNS cancer (astro) SNB-75	0.0
Lung ca. NCI-H146	0.0	CNS cancer (glio) SNB-19	0.0
Lung ca. SHP-77	0.0	CNS cancer (glio) SF-295	0.2
Lung ca. A549	0.0	Brain (Amygdala) Pool	0.2
Lung ca. NCI-H526	1.0	Brain (cerebellum)	0.0
Lung ca. NCI-H23	0.0	Brain (fetal)	0.6
Lung ca. NCI-H460	0.0	Brain (Hippocampus) Pool	0.0
Lung ca. HOP-62	0.0	Cerebral Cortex Pool	0.2
Lung ca. NCI-H522	0.0	Brain (Substantia nigra) Pool	0.0
Liver	0.0	Brain (Thalamus) Pool	0.0
Fetal Liver	0.0	Brain (whole)	0.0
Liver ca. HepG2	0.0	Spinal Cord Pool	0.0
Kidney Pool	0.0	Adrenal Gland	0.0
Fetal Kidney	0.0	Pituitary gland Pool	0.0
Renal ca. 786-0	1.6	Salivary Gland	0.0
Renal ca. A498	0.0	Thyroid (female)	0.2
Renal ca. ACHN	0.0	Pancreatic ca. CAPAN2	0.0
Renal ca. UO-31	0.0	Pancreas Pool	0.0

Table BCC. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag3544, Run 169850546	Tissue Name	Rel. Exp.(%) Ag3544, Run 169850546
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Secondary Th1 act	0.0	HUVEC IL-1beta	0.0
Secondary Th2 act	0.0	HUVEC IFN gamma	0.0
Secondary Tr1 act	0.0	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	0.0	HUVEC IL-11	0.0
Secondary Tr1 rest	0.0	Lung Microvascular EC none	0.0
Primary Th1 act	0.0	Lung Microvascular EC TNFalpha + IL-1beta	0.0
Primary Th2 act	0.0	Microvascular Dermal EC none	0.0
Primary Tr1 act	0.0	Microvascular Dermal EC TNFalpha + IL-1beta	0.0
Primary Th1 rest	2.6	Bronchial epithelium TNFalpha + IL1beta	0.0
Primary Th2 rest	0.0	Small airway epithelium none	0.0
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	0.0
CD45RA CD4 lymphocyte act	0.0	Coronary artery SMC rest	0.0
CD45RO CD4 lymphocyte act	0.0	Coronary artery SMC TNFalpha + IL-1beta	0.0
CD8 lymphocyte act	0.0	Astrocytes rest	0.0
Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFalpha + IL-1beta	0.0
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	100.0
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	61.1
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.0	CCD1106 (Keratinocytes) none	0.0
LAK cells rest	0.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0
LAK cells IL-2	0.0	Liver cirrhosis	0.0
LAK cells IL-2+IL-12	0.0	NCI-H292 none	0.0
LAK cells IL-2+IFN gamma	0.0	NCI-H292 IL-4	0.0
LAK cells IL-2+ IL-18	0.0	NCI-H292 IL-9	0.0
LAK cells PMA/ionomycin	0.0	NCI-H292 IL-13	0.0
NK Cells IL-2 rest	0.0	NCI-H292 IFN gamma	0.0
Two Way MLR 3 day	0.0	HPAEC none	0.0
Two Way MLR 5 day	0.0	HPAEC TNF alpha + IL-1	0.0

		beta	
Two Way MLR 7 day	0.0	Lung fibroblast none	0.0
PBMC rest	0.0	Lung fibroblast TNF alpha + IL-1 beta	0.0
PBMC PWM	0.0	Lung fibroblast IL-4	0.0
PBMC PHA-L	0.0	Lung fibroblast IL-9	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-13	0.0
Ramos (B cell) ionomycin	0.0	Lung fibroblast IFN gamma	0.0
B lymphocytes PWM	0.0	Dermal fibroblast CCD1070 rest	0.0
B lymphocytes CD40L and IL-4	0.0	Dermal fibroblast CCD1070 TNF alpha	0.0
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 IL-1 beta	0.0
EOL-1 dbcAMP PMA/ionomycin	0.0	Dermal fibroblast IFN gamma	0.0
Dendritic cells none	0.0	Dermal fibroblast IL-4	0.0
Dendritic cells LPS	0.0	Dermal Fibroblasts rest	0.0
Dendritic cells anti- CD40	0.0	Neutrophils TNFa+LPS	0.0
Monocytes rest	0.0	Neutrophils rest	0.0
Monocytes LPS	0.0	Colon	0.0
Macrophages rest	0.0	Lung	0.0
Macrophages LPS	0.0	Thymus	0.0
HUVEC none	0.0	Kidney	0.0
HUVEC starved	0.0		

CNS_neurodegeneration_v1.0 Summary: Ag3544 Expression of the CG59319-02 gene is low/undetectable in all samples on this panel (CTs>35). (Data not shown.)

General_screening_panel_v1.4 Summary: Ag3544 Expression of the CG59319-02 gene is restricted to a sample derived from the testis (CT=29.8). Thus, expression of this gene could be used to differentiate between this sample and other samples on this panel and as a marker of testicular tissue. Furthermore, therapeutic modulation of the expression or function of this gene may be useful in the treatment of male infertility or hypogonadism.

Panel 4.1D Summary: Ag3544 Expression of the CG59319-02 gene is restricted to samples derived from the basophil cell line KU-812 (CTs=32). Thus, expression of this gene could be used as a marker of this cell type. Furthermore, the specific pattern of expression of this gene suggests that therapeutic modulation of the expression or function of the protein encoded by

this gene may block or inhibit inflammation or tissue damage due to basophil activation in response to asthma, allergies, hypersensitivity reactions, psoriasis, and viral infections.

BD. CG59576-01: Olfactory Receptor

Expression of gene CG59576-01 was assessed using the primer-probe set Ag3478, described in Table BDA. Results of the RTQ-PCR runs are shown in Table BDB.

Table BDA. Probe Name Ag3478

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-tggaagtgtagccctgatgtac-3'	22	708	562
Probe	TET-5'-tgctcttctctgccaagtactccttt-3'- TAMRA	26	731	563
Reverse	5'-aaacattaggctgatggttg-3'	22	765	564

Table BDB. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3478, Run 166441540	Tissue Name	Rel. Exp.(%) Ag3478, Run 166441540
Secondary Th1 act	0.0	HUVEC IL-1beta	0.0
Secondary Th2 act	0.0	HUVEC IFN gamma	0.0
Secondary Tr1 act	0.0	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	9.0	HUVEC IL-11	0.0
Secondary Tr1 rest	0.0	Lung Microvascular EC none	0.0
Primary Th1 act	0.0	Lung Microvascular EC TNFalpha + IL-1beta	0.0
Primary Th2 act	0.0	Microvascular Dermal EC none	0.0
Primary Tr1 act	0.0	Microvascular Dermal EC TNFalpha + IL-1beta	0.0
Primary Th1 rest	0.0	Bronchial epithelium TNFalpha + IL1beta	0.0
Primary Th2 rest	0.0	Small airway epithelium none	0.0
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	0.0
CD45RA CD4 lymphocyte act	0.0	Coronary artery SMC rest	0.0

CD45RO CD4 lymphocyte act	0.0	Coronary artery SMC TNFalpha + IL-1beta	0.0
CD8 lymphocyte act	0.0	Astrocytes rest	0.0
Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFalpha + IL-1beta	0.0
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	4.6
2ry Th1/Th2/Tr1_anti-CD95 CH11	2.6	CCD1106 (Keratinocytes) none	0.0
LAK cells rest	0.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0
LAK cells IL-2	0.0	Liver cirrhosis	100.0
LAK cells IL-2+IL-12	0.0	Lupus kidney	0.0
LAK cells IL-2+IFN gamma	0.0	NCI-H292 none	0.0
LAK cells IL-2+ IL-18	0.0	NCI-H292 IL-4	0.0
LAK cells PMA/ionomycin	0.0	NCI-H292 IL-9	0.0
NK Cells IL-2 rest	0.0	NCI-H292 IL-13	0.0
Two Way MLR 3 day	0.0	NCI-H292 IFN gamma	0.0
Two Way MLR 5 day	0.0	HPAEC none	0.0
Two Way MLR 7 day	0.0	HPAEC TNF alpha + IL-1 beta	0.0
PBMC rest	0.0	Lung fibroblast none	0.0
PBMC PWM	0.0	Lung fibroblast TNF alpha + IL-1 beta	0.0
PBMC PHA-L	0.0	Lung fibroblast IL-4	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-9	0.0
Ramos (B cell) ionomycin	0.0	Lung fibroblast IL-13	0.0
B lymphocytes PWM	0.0	Lung fibroblast IFN gamma	0.0
B lymphocytes CD40L and IL-4	0.0	Dermal fibroblast CCD1070 rest	0.0
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 TNF alpha	0.0
EOL-1 dbcAMP PMA/ionomycin	0.0	Dermal fibroblast CCD1070 IL-1 beta	0.0
Dendritic cells none	0.0	Dermal fibroblast IFN gamma	0.0
Dendritic cells LPS	0.0	Dermal fibroblast IL-4	0.0
Dendritic cells anti-CD40	0.0	IBD Colitis 2	25.7

Monocytes rest	0.0	IBD Crohn's	24.3
Monocytes LPS	0.0	Colon	5.9
Macrophages rest	0.0	Lung	5.8
Macrophages LPS	0.0	Thymus	5.9
HUVEC none	0.0	Kidney	10.2
HUVEC starved	0.0		

CNS_neurodegeneration_v1.0 Summary: Ag3478 Expression of the CG59576-01 gene is low/undetectable in all samples on this panel (CTs>35). (Data not shown.)

General_screening_panel_v1.4 Summary: Ag3478 Expression of the CG59576-01 gene is low/undetectable in all samples on this panel (CTs>35). (Data not shown.)

General_screening_panel_v1.5 Summary: Ag3478 Expression of the CG59576-01 gene is low/undetectable in all samples on this panel (CTs>35). (Data not shown.)

Panel 4D Summary: Ag3478 Expression of the CG59576-01 gene is restricted to a sample derived from liver cirrhosis (CT=32.3). Furthermore, expression of this gene is not detected in normal liver in Panel 1.4, suggesting that its expression is unique to liver cirrhosis. This gene encodes a putative GPCR; therefore, antibodies or small molecule therapeutics could reduce or inhibit fibrosis that occurs in liver cirrhosis. In addition, antibodies to this putative GPCR could also be used for the diagnosis of liver cirrhosis.

Panel 5 Islet Summary: Ag3478 Expression of the CG59576-01 gene is low/undetectable in all samples on this panel (CTs>35). (Data not shown.)

BE. CG59557-01: Olfactory Receptor

Expression of gene CG59557-01 was assessed using the primer-probe set Ag3470, described in Table BEA. Results of the RTQ-PCR runs are shown in Table BEB.

Table BEA. Probe Name Ag3470

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-ccaaccttctcagtgaacagaa-3'	22	413	565
Probe	TET-5'-tctctttcataggttgccctcctgcaga-3'- TAMRA	27	440	566
Reverse	5'-ccgagtgagtgaagaagtaca-3'	22	467	567

Table BEB. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3470, Run 166417125	Tissue Name	Rel. Exp.(%) Ag3470, Run 166417125
Secondary Th1 act	0.0	HUVEC IL-1beta	0.0
Secondary Th2 act	3.2	HUVEC IFN gamma	0.0
Secondary Tr1 act	0.0	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	0.0	HUVEC IL-11	0.0
Secondary Tr1 rest	0.0	Lung Microvascular EC none	0.0
Primary Th1 act	0.0	Lung Microvascular EC TNFalpha + IL-1beta	3.0
Primary Th2 act	0.0	Microvascular Dermal EC none	0.0
Primary Tr1 act	0.0	Microvascular Dermal EC TNFalpha + IL-1beta	0.0
Primary Th1 rest	2.8	Bronchial epithelium TNFalpha + IL1beta	0.0
Primary Th2 rest	0.0	Small airway epithelium none	0.0
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	0.0
CD45RA CD4 lymphocyte act	0.0	Coronary artery SMC rest	0.0
CD45RO CD4 lymphocyte act	0.0	Coronary artery SMC TNFalpha + IL-1beta	0.0
CD8 lymphocyte act	0.0	Astrocytes rest	0.0
Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFalpha + IL-1beta	0.0
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	2.9	KU-812 (Basophil) PMA/ionomycin	0.0
2ry Th1/Th2/Tr1_anti- CD95 CH11	0.0	CCD1106 (Keratinocytes) none	0.0
LAK cells rest	0.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0
LAK cells IL-2	0.0	Liver cirrhosis	100.0
LAK cells IL-2+IL-12	0.0	Lupus kidney	2.2
LAK cells IL-2+IFN gamma	0.0	NCI-H292 none	0.0
LAK cells IL-2+ IL-18	3.2	NCI-H292 IL-4	0.0

LAK cells PMA/ionomycin	0.0	NCI-H292 IL-9	0.0
NK Cells IL-2 rest	0.0	NCI-H292 IL-13	0.0
Two Way MLR 3 day	0.0	NCI-H292 IFN gamma	0.0
Two Way MLR 5 day	0.0	HPAEC none	0.0
Two Way MLR 7 day	0.0	HPAEC TNF alpha + IL-1 beta	0.0
PBMC rest	5.8	Lung fibroblast none	0.0
PBMC PWM	2.7	Lung fibroblast TNF alpha + IL-1 beta	0.0
PBMC PHA-L	0.0	Lung fibroblast IL-4	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-9	0.0
Ramos (B cell) ionomycin	0.0	Lung fibroblast IL-13	0.0
B lymphocytes PWM	6.5	Lung fibroblast IFN gamma	0.0
B lymphocytes CD40L and IL-4	2.2	Dermal fibroblast CCD1070 rest	0.0
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 TNF alpha	0.0
EOL-1 dbcAMP PMA/ionomycin	0.0	Dermal fibroblast CCD1070 IL-1 beta	0.0
Dendritic cells none	3.2	Dermal fibroblast IFN gamma	0.0
Dendritic cells LPS	20.9	Dermal fibroblast IL-4	0.0
Dendritic cells anti- CD40	0.0	IBD Colitis 2	19.6
Monocytes rest	0.0	IBD Crohn's	4.9
Monocytes LPS	6.3	Colon	13.9
Macrophages rest	21.6	Lung	14.8
Macrophages LPS	0.0	Thymus	2.2
HUVEC none	0.0	Kidney	0.0
HUVEC starved	0.0		

CNS_neurodegeneration_v1.0 Summary: Ag3470 Expression of the CG59557-01 gene is low/undetectable in all samples on this panel (CTs>35). (Data not shown.)

General_screening_panel_v1.4 Summary: Ag3470 Expression of the CG59557-01 gene is low/undetectable in all samples on this panel (CTs>35). (Data not shown.)

Panel 4D Summary: Ag3470 Expression of the CG59557-01 gene is detected in a liver cirrhosis sample (CT = 32.2). Furthermore, expression of this gene is not detected in normal liver in Panel 1.4, suggesting that its expression is unique to liver cirrhosis. This gene encodes

a putative GPCR; therefore, antibodies or small molecule therapeutics could reduce or inhibit fibrosis that occurs in liver cirrhosis. In addition, antibodies to this putative GPCR could also be used for the diagnosis of liver cirrhosis.

BF. CG59555-01: Olfactory Receptor

Expression of gene CG59555-01 was assessed using the primer-probe set Ag3467, described in Table BFA. Results of the RTQ-PCR runs are shown in Tables BFB, BFC and BFD.

Table BFA. Probe Name Ag3467

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-ggcaaggaaagtcattcctaa-3'	21	953	568
Probe	TET-5'-tggtgtgacatttgactctccctcct-3'- TAMRA	26	975	569
Reverse	5'-tggtaccaagattccaggagat-3'	22	1006	570

Table BFB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3467, Run 210376517	Tissue Name	Rel. Exp.(%) Ag3467, Run 210376517
AD 1 Hippo	4.6	Control (Path) 3 Temporal Ctx	14.8
AD 2 Hippo	29.7	Control (Path) 4 Temporal Ctx	15.2
AD 3 Hippo	10.7	AD 1 Occipital Ctx	14.5
AD 4 Hippo	28.9	AD 2 Occipital Ctx (Missing)	0.0
AD 5 hippo	21.6	AD 3 Occipital Ctx	14.5
AD 6 Hippo	100.0	AD 4 Occipital Ctx	14.8
Control 2 Hippo	8.8	AD 5 Occipital Ctx	13.7
Control 4 Hippo	35.6	AD 6 Occipital Ctx	10.3
Control (Path) 3 Hippo	21.9	Control 1 Occipital Ctx	18.3
AD 1 Temporal Ctx	28.3	Control 2 Occipital Ctx	7.9
AD 2 Temporal Ctx	37.4	Control 3 Occipital Ctx	16.2
AD 3 Temporal Ctx	7.4	Control 4 Occipital Ctx	24.0
AD 4 Temporal Ctx	28.3	Control (Path) 1	28.3

		Occipital Ctx	
AD 5 Inf Temporal Ctx	19.3	Control (Path) 2 Occipital Ctx	10.1
AD 5 Sup Temporal Ctx	33.4	Control (Path) 3 Occipital Ctx	12.6
AD 6 Inf Temporal Ctx	39.8	Control (Path) 4 Occipital Ctx	14.3
AD 6 Sup Temporal Ctx	83.5	Control 1 Parietal Ctx	8.7
Control 1 Temporal Ctx	14.4	Control 2 Parietal Ctx	22.2
Control 2 Temporal Ctx	13.6	Control 3 Parietal Ctx	9.8
Control 3 Temporal Ctx	11.8	Control (Path) 1 Parietal Ctx	33.2
Control 4 Temporal Ctx	16.0	Control (Path) 2 Parietal Ctx	12.4
Control (Path) 1 Temporal Ctx	24.3	Control (Path) 3 Parietal Ctx	19.6
Control (Path) 2 Temporal Ctx	6.1	Control (Path) 4 Parietal Ctx	12.9

Table BFC. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3467, Run 217119371	Tissue Name	Rel. Exp.(%) Ag3467, Run 217119371
Adipose	11.6	Renal ca. TK-10	14.6
Melanoma* Hs688(A).T	27.0	Bladder	14.1
Melanoma* Hs688(B).T	27.9	Gastric ca. (liver met.) NCI-N87	3.2
Melanoma* M14	11.2	Gastric ca. KATO III	2.1
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.4
Melanoma* SK-MEL-5	0.0	Colon ca. SW480	12.7
Squamous cell carcinoma SCC-4	1.8	Colon ca.* (SW480 met) SW620	10.4
Testis Pool	7.0	Colon ca. HT29	1.7
Prostate ca.* (bone met) PC-3	15.2	Colon ca. HCT-116	7.9
Prostate Pool	9.7	Colon ca. CaCo-2	5.3
Placenta	1.7	Colon cancer tissue	3.6
Uterus Pool	5.1	Colon ca. SW1116	0.4
Ovarian ca.	4.1	Colon ca. Colo-205	0.2

OVCAR-3			
Ovarian ca. SK-OV-3	16.2	Colon ca. SW-48	0.5
Ovarian ca. OVCAR-4	5.2	Colon Pool	20.6
Ovarian ca. OVCAR-5	13.9	Small Intestine Pool	26.8
Ovarian ca. IGROV-1	0.0	Stomach Pool	19.5
Ovarian ca. OVCAR-8	9.5	Bone Marrow Pool	16.7
Ovary	8.4	Fetal Heart	23.5
Breast ca. MCF-7	0.8	Heart Pool	11.2
Breast ca. MDA-MB-231	26.2	Lymph Node Pool	31.9
Breast ca. BT 549	0.0	Fetal Skeletal Muscle	7.1
Breast ca. T47D	18.2	Skeletal Muscle Pool	1.8
Breast ca. MDA-N	10.9	Spleen Pool	22.4
Breast Pool	26.6	Thymus Pool	25.9
Trachea	9.5	CNS cancer (glio/astro) U87-MG	0.4
Lung	12.4	CNS cancer (glio/astro) U-118-MG	0.2
Fetal Lung	100.0	CNS cancer (neuro;met) SK-N-AS	0.0
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF-539	0.0
Lung ca. LX-1	11.6	CNS cancer (astro) SNB-75	1.5
Lung ca. NCI-H146	0.0	CNS cancer (glio) SNB-19	1.1
Lung ca. SHP-77	0.1	CNS cancer (glio) SF-295	20.0
Lung ca. A549	3.0	Brain (Amygdala) Pool	1.9
Lung ca. NCI-H526	0.0	Brain (cerebellum)	1.0
Lung ca. NCI-H23	13.9	Brain (fetal)	2.5
Lung ca. NCI-H460	5.4	Brain (Hippocampus) Pool	0.2
Lung ca. HOP-62	6.7	Cerebral Cortex Pool	1.3
Lung ca. NCI-H522	0.0	Brain (Substantia nigra) Pool	1.6
Liver	0.1	Brain (Thalamus) Pool	2.5
Fetal Liver	6.6	Brain (whole)	1.1
Liver ca. HepG2	1.4	Spinal Cord Pool	4.5

Kidney Pool	34.4	Adrenal Gland	6.3
Fetal Kidney	76.3	Pituitary gland Pool	4.5
Renal ca. 786-0	28.1	Salivary Gland	1.8
Renal ca. A498	12.1	Thyroid (female)	13.4
Renal ca. ACHN	23.0	Pancreatic ca. CAPAN2	1.0
Renal ca. UO-31	25.0	Pancreas Pool	27.2

Table BFD. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3467, Run 166417105	Tissue Name	Rel. Exp.(%) Ag3467, Run 166417105
Secondary Th1 act	2.4	HUVEC IL-1beta	1.5
Secondary Th2 act	5.1	HUVEC IFN gamma	18.2
Secondary Tr1 act	7.2	HUVEC TNF alpha + IFN gamma	6.2
Secondary Th1 rest	18.2	HUVEC TNF alpha + IL4	1.7
Secondary Th2 rest	14.6	HUVEC IL-11	1.8
Secondary Tr1 rest	22.1	Lung Microvascular EC none	0.6
Primary Th1 act	1.3	Lung Microvascular EC TNFalpha + IL-1beta	0.3
Primary Th2 act	9.0	Microvascular Dermal EC none	0.1
Primary Tr1 act	7.2	Microvascular Dermal EC TNFalpha + IL-1beta	0.5
Primary Th1 rest	100.0	Bronchial epithelium TNFalpha + IL1beta	1.5
Primary Th2 rest	38.7	Small airway epithelium none	1.6
Primary Tr1 rest	28.1	Small airway epithelium TNFalpha + IL-1beta	6.6
CD45RA CD4 lymphocyte act	1.9	Coronary artery SMC rest	4.5
CD45RO CD4 lymphocyte act	8.7	Coronary artery SMC TNFalpha + IL-1beta	5.1
CD8 lymphocyte act	4.0	Astrocytes rest	0.4
Secondary CD8 lymphocyte rest	7.5	Astrocytes TNFalpha + IL-1beta	1.7
Secondary CD8 lymphocyte act	4.7	KU-812 (Basophil) rest	0.7
CD4 lymphocyte none	9.3	KU-812 (Basophil) PMA/ionomycin	3.2
2ry Th1/Th2/Tr1_anti-	52.5	CCD1106 (Keratinocytes)	1.5

CD95 CH11		none	
LAK cells rest	4.6	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	16.4
LAK cells IL-2	15.1	Liver cirrhosis	14.6
LAK cells IL-2+IL-12	6.5	Lupus kidney	37.6
LAK cells IL-2+IFN gamma	10.9	NCI-H292 none	4.6
LAK cells IL-2+ IL-18	6.9	NCI-H292 IL-4	5.2
LAK cells PMA/ionomycin	1.1	NCI-H292 IL-9	5.6
NK Cells IL-2 rest	3.1	NCI-H292 IL-13	2.3
Two Way MLR 3 day	11.0	NCI-H292 IFN gamma	1.5
Two Way MLR 5 day	6.0	HPAEC none	3.6
Two Way MLR 7 day	6.7	HPAEC TNF alpha + IL-1 beta	10.5
PBMC rest	2.6	Lung fibroblast none	15.3
PBMC PWM	4.2	Lung fibroblast TNF alpha + IL-1 beta	5.9
PBMC PHA-L	3.1	Lung fibroblast IL-4	5.6
Ramos (B cell) none	0.0	Lung fibroblast IL-9	5.6
Ramos (B cell) ionomycin	0.1	Lung fibroblast IL-13	5.1
B lymphocytes PWM	6.0	Lung fibroblast IFN gamma	7.9
B lymphocytes CD40L and IL-4	6.5	Dermal fibroblast CCD1070 rest	4.5
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 TNF alpha	21.6
EOL-1 dbcAMP PMA/ionomycin	0.0	Dermal fibroblast CCD1070 IL-1 beta	2.0
Dendritic cells none	0.4	Dermal fibroblast IFN gamma	3.5
Dendritic cells LPS	0.1	Dermal fibroblast IL-4	6.9
Dendritic cells anti- CD40	0.1	IBD Colitis 2	10.6
Monocytes rest	1.6	IBD Crohn's	1.8
Monocytes LPS	1.7	Colon	34.9
Macrophages rest	8.4	Lung	6.7
Macrophages LPS	1.2	Thymus	26.8
HUVEC none	2.6	Kidney	11.3
HUVEC starved	2.8		

CNS_neurodegeneration_v1.0 Summary: Ag3467 The CG59555-01 gene encodes a putative GPCR. It is expressed at low to moderate levels in most of the samples used in this

panel. This panel confirms the expression of CG59555-01 gene at low levels in the brains of an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. Please see Panel 1.4 for a discussion of the potential utility of this gene in treatment of central nervous system disorders.

General_screening_panel_v1.4 Summary: Ag3467 The CG59555-01 gene encodes a putative GPCR. It is expressed at low to moderate levels in large number of the samples used in this panel. Highest expression of this gene is detected in fetal lung (CT=28). Interestingly, this gene is expressed at much higher levels in fetal (CT = 28) when compared to adult lung (CT = 31). Therefore, expression of this gene can be used to distinguish fetal lung from adult lung and from other samples used in this panel. In addition, this gene is also expressed at much higher levels in fetal fetal liver (CT=32) as compared to adult liver (CT=38). Thus, expression of this gene can be used to distinguish fetal liver from adult liver.

Among tissues with metabolic or endocrine function, this gene is expressed at low to moderate levels in pancreas, adipose, adrenal gland, thyroid, pituitary gland, skeletal muscle, heart, liver and the gastrointestinal tract. Therefore, therapeutic modulation of the activity of this gene may prove useful in the treatment of endocrine/metabolically related diseases, such as obesity and diabetes.

This gene is also expressed at low levels in all regions of the central nervous system examined, including amygdala, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord. Several neurotransmitter receptors are GPCRs, including the dopamine receptor family, the serotonin receptor family, the GABAB receptor, muscarinic acetylcholine receptors, and others; thus this GPCR may represent a novel neurotransmitter receptor. Targeting various neurotransmitter receptors (dopamine, serotonin) has proven to be an effective therapy in psychiatric illnesses such as schizophrenia, bipolar disorder, and depression. Furthermore, the cerebral cortex and hippocampus are regions of the brain that are known to be involved in Alzheimer's disease, seizure disorders, and in the normal process of memory formation. Therefore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

Panel 4D Summary: Ag3467 The CG59555-01 gene encodes a putative GPCR. Highest expression of this gene is detected in resting primary Th1 cells (CT=27). This gene is expressed at moderate levels in a wide range of cell types of significance in the immune response in health and disease. These cells include members of the T-cell, B-cell, endothelial cell, macrophage/monocyte, and peripheral blood mononuclear cell family, as well as epithelial and fibroblast cell types from lung and skin, and normal tissues represented by colon, lung, thymus and kidney. This ubiquitous pattern of expression suggests that this gene product may be involved in homeostatic processes for these and other cell types and tissues. This pattern is in agreement with the expression profile in General_screening_panel_v1.4 and also suggests a role for the gene product in cell survival and proliferation. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

BG. CG59551-01: Olfactory Receptor

Expression of gene CG59551-01 was assessed using the primer-probe set Ag3463, described in Table BGA. Results of the RTQ-PCR runs are shown in Tables BGB and BGC.

Table BGA. Probe Name Ag3463

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-ctatgggtttccagatgtttcca-3'	22	78	571
Probe	TET-5'-tagatgttccagctgcccatctctga-3'-TAMRA	26	105	572
Reverse	5'-attgtgagacacagctggattt-3'	22	132	573

Table BGB. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3463, Run 217067349	Tissue Name	Rel. Exp.(%) Ag3463, Run 217067349
Adipose	0.0	Renal ca. TK-10	9.0
Melanoma* Hs688(A).T	0.0	Bladder	11.2
Melanoma* Hs688(B).T	0.0	Gastric ca. (liver met.) NCI-N87	13.0
Melanoma* M14	0.0	Gastric ca. KATO III	0.0

Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.0
Melanoma* SK- MEL-5	43.8	Colon ca. SW480	11.6
Squamous cell carcinoma SCC-4	0.0	Colon ca.* (SW480 met) SW620	0.0
Testis Pool	85.9	Colon ca. HT29	0.0
Prostate ca.* (bone met) PC-3	0.0	Colon ca. HCT-116	10.7
Prostate Pool	7.2	Colon ca. CaCo-2	12.8
Placenta	12.8	Colon cancer tissue	0.0
Uterus Pool	0.0	Colon ca. SW1116	0.0
Ovarian ca. OVCA-3	0.0	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV- 3	100.0	Colon ca. SW-48	0.0
Ovarian ca. OVCA-4	11.9	Colon Pool	12.5
Ovarian ca. OVCA-5	11.3	Small Intestine Pool	0.0
Ovarian ca. IGROV- 1	26.1	Stomach Pool	0.0
Ovarian ca. OVCA-8	0.0	Bone Marrow Pool	0.0
Ovary	0.0	Fetal Heart	0.0
Breast ca. MCF-7	0.0	Heart Pool	0.0
Breast ca. MDA- MB-231	0.0	Lymph Node Pool	23.2
Breast ca. BT 549	20.3	Fetal Skeletal Muscle	82.9
Breast ca. T47D	0.0	Skeletal Muscle Pool	0.0
Breast ca. MDA-N	31.9	Spleen Pool	0.0
Breast Pool	12.5	Thymus Pool	0.0
Trachea	20.9	CNS cancer (glio/astro) U87-MG	0.0
Lung	0.0	CNS cancer (glio/astro) U-118-MG	24.0
Fetal Lung	23.7	CNS cancer (neuro;met) SK-N-AS	0.0
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF- 539	0.0
Lung ca. LX-1	0.0	CNS cancer (astro) SNB-75	38.2
Lung ca. NCI-H146	0.0	CNS cancer (glio) SNB-19	0.0
Lung ca. SHP-77	8.8	CNS cancer (glio) SF-	33.2

		295	
Lung ca. A549	0.0	Brain (Amygdala) Pool	0.0
Lung ca. NCI-H526	0.0	Brain (cerebellum)	0.0
Lung ca. NCI-H23	57.4	Brain (fetal)	48.6
Lung ca. NCI-H460	31.2	Brain (Hippocampus) Pool	21.3
Lung ca. HOP-62	0.0	Cerebral Cortex Pool	35.6
Lung ca. NCI-H522	14.4	Brain (Substantia nigra) Pool	15.5
Liver	0.0	Brain (Thalamus) Pool	14.1
Fetal Liver	0.0	Brain (whole)	0.0
Liver ca. HepG2	5.0	Spinal Cord Pool	29.5
Kidney Pool	37.9	Adrenal Gland	14.8
Fetal Kidney	0.0	Pituitary gland Pool	0.0
Renal ca. 786-0	0.0	Salivary Gland	0.0
Renal ca. A498	0.0	Thyroid (female)	0.0
Renal ca. ACHN	0.0	Pancreatic ca. CAPAN2	0.0
Renal ca. UO-31	0.0	Pancreas Pool	12.2

Table BGC. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag3463, Run 169839351	Tissue Name	Rel. Exp.(%) Ag3463, Run 169839351
Secondary Th1 act	0.0	HUVEC IL-1beta	0.0
Secondary Th2 act	0.0	HUVEC IFN gamma	0.0
Secondary Tr1 act	1.3	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	2.6	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	0.0	HUVEC IL-11	0.0
Secondary Tr1 rest	0.0	Lung Microvascular EC none	0.0
Primary Th1 act	0.0	Lung Microvascular EC TNFalpha + IL-1beta	0.0
Primary Th2 act	0.0	Microvascular Dermal EC none	0.0
Primary Tr1 act	0.0	Microvascular Dermal EC TNFalpha + IL-1beta	1.4
Primary Th1 rest	0.0	Bronchial epithelium TNFalpha + IL1beta	0.6
Primary Th2 rest	0.0	Small airway epithelium none	0.0
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	0.0

CD45RA CD4 lymphocyte act	0.0	Coronary artery SMC rest	0.0
CD45RO CD4 lymphocyte act	0.0	Coronary artery SMC TNFalpha + IL-1beta	0.0
CD8 lymphocyte act	0.0	Astrocytes rest	0.0
Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFalpha + IL-1beta	0.0
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	7.2
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	100.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.0	CCD1106 (Keratinocytes) none	0.0
LAK cells rest	0.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	1.1
LAK cells IL-2	0.0	Liver cirrhosis	1.2
LAK cells IL-2+IL-12	0.0	NCI-H292 none	0.0
LAK cells IL-2+IFN gamma	0.0	NCI-H292 IL-4	0.0
LAK cells IL-2+ IL-18	0.0	NCI-H292 IL-9	0.0
LAK cells PMA/ionomycin	0.0	NCI-H292 IL-13	0.0
NK Cells IL-2 rest	0.0	NCI-H292 IFN gamma	0.0
Two Way MLR 3 day	1.3	HPAEC none	1.2
Two Way MLR 5 day	0.0	HPAEC TNF alpha + IL-1 beta	0.0
Two Way MLR 7 day	0.0	Lung fibroblast none	1.0
PBMC rest	0.0	Lung fibroblast TNF alpha + IL-1 beta	0.0
PBMC PWM	0.0	Lung fibroblast IL-4	0.0
PBMC PHA-L	0.0	Lung fibroblast IL-9	0.0
Ramos (B cell) none	1.3	Lung fibroblast IL-13	0.0
Ramos (B cell) ionomycin	0.0	Lung fibroblast IFN gamma	0.0
B lymphocytes PWM	0.0	Dermal fibroblast CCD1070 rest	0.0
B lymphocytes CD40L and IL-4	1.2	Dermal fibroblast CCD1070 TNF alpha	0.0
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 IL-1 beta	0.0
EOL-1 dbcAMP PMA/ionomycin	0.0	Dermal fibroblast IFN gamma	0.0
Dendritic cells none	6.1	Dermal fibroblast IL-4	0.0
Dendritic cells LPS	0.0	Dermal Fibroblasts rest	0.0

Dendritic cells anti-CD40	1.2	Neutrophils TNFa+LPS	0.0
Monocytes rest	0.0	Neutrophils rest	0.0
Monocytes LPS	0.0	Colon	0.5
Macrophages rest	4.1	Lung	0.0
Macrophages LPS	0.0	Thymus	0.0
HUVEC none	0.0	Kidney	2.3
HUVEC starved	0.0		

CNS_neurodegeneration_v1.0 Summary: Ag3463 Expression of the CG59551-01 gene is low/undetectable in all the samples on this panel. (Data not shown.)

General_screening_panel_v1.4 Summary: Ag3463 The CG59551-01 gene encodes a putative GPCR. Highest expression of this gene is detected in an ovarian cancer cell line SK-OV-3 (CT=34). In addition, low expression of this gene is also observed in fetal skeletal muscle (CT= 34.4), one of the lung cancer cell line (CT= 34.9), and testis (CT= 34.3). Thus, expression of this gene can be used to distinguish these sample from other samples used in this panel. In addition, therapeutic modulation of the activity of the GPCR encoded by this gene may be useful in the treatment of ovarian and lung cancer, fertility, hypogonadism, and muscle related diseases.

Panel 4.1D Summary: Ag3463 The CG59551-01 gene encodes a putative GPCR. Highest expression of this gene is seen in KU-812 cells treated with PMA/ionomycin (CT=30.86). Thus, expression of this gene can be used to distinguish this sample from other samples used in this panel. In addition, expression of this gene is high in KU-812 (basophils) cells treated with PMA/ionomycin (CT=30.86) as compared to resting KU-812 cells (CT=34.66). Therefore, expression of this gene can be used to distinguish resting from PMA/ionomycin treated- basophils. It is known that GPCR-type receptors are important in multiple physiological responses mediated by basophils (ref. 1). Therefore, antibody or small molecule therapies designed with the protein encoded for by this gene could block or inhibit inflammation or tissue damage due to basophil activation in response to asthma, allergies, hypersensitivity reactions, psoriasis, and viral infections.

References:

1. Heinemann A., Hartnell A., Stubbs V.E., Murakami K., Soler D., LaRosa G., Askenase P.W., Williams T.J., Sabroe I. (2000) Basophil responses to chemokines are regulated by both sequential and cooperative receptor signaling. J. Immunol. 165: 7224-7233.

BH. CG59540-01: OLFACTORY RECEPTOR

Expression of gene CG59540-01 was assessed using the primer-probe sets Ag3460 and Ag1519, described in Tables BHA and BHB. Results of the RTQ-PCR runs are shown in Tables BHC, BHD and BHE.

Table BHA. Probe Name Ag3460

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-tcagtgcagagatggagatctt-3'	22	97	574
Probe	TET-5'-tgcattcttctccctgttatatctcttca-3'- TAMRA	28	126	575
Reverse	5'-gacagatgagtcacctgttcat-3'	22	171	576

Table BHB. Probe Name Ag1519

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-cctggccctcataaatctaatt-3'	22	503	577
Probe	TET-5'-ctccttctaaggctgcccttctgtgg-3'- TAMRA	26	525	578
Reverse	5'-acagacagaatttcaccgaaga-3'	22	571	579

Table BHC. Panel 1.2

Tissue Name	Rel. Exp.(%) Ag1519, Run 142098791	Tissue Name	Rel. Exp.(%) Ag1519, Run 142098791
Endothelial cells	0.0	Renal ca. 786-0	32.1
Heart (Fetal)	1.3	Renal ca. A498	10.7
Pancreas	1.5	Renal ca. RXF 393	7.5
Pancreatic ca. CAPAN 2	3.6	Renal ca. ACHN	10.2
Adrenal Gland	4.7	Renal ca. UO-31	26.8
Thyroid	0.4	Renal ca. TK-10	14.0
Salivary gland	27.7	Liver	7.2
Pituitary gland	0.0	Liver (fetal)	3.5
Brain (fetal)	0.0	Liver ca. (hepatoblast) HepG2	0.9

Brain (whole)	0.0	Lung	0.0
Brain (amygdala)	0.0	Lung (fetal)	1.3
Brain (cerebellum)	0.0	Lung ca. (small cell) LX-1	22.8
Brain (hippocampus)	0.3	Lung ca. (small cell) NCI-H69	11.5
Brain (thalamus)	0.2	Lung ca. (s.cell var.) SHP-77	0.0
Cerebral Cortex	0.3	Lung ca. (large cell)NCI-H460	2.3
Spinal cord	0.0	Lung ca. (non-sm. cell) A549	5.1
glio/astro U87-MG	0.4	Lung ca. (non-s.cell) NCI-H23	7.7
glio/astro U-118-MG	0.9	Lung ca. (non-s.cell) HOP-62	6.8
astrocytoma SW1783	0.0	Lung ca. (non-s.cl) NCI-H522	0.9
neuro*; met SK-N-AS	0.0	Lung ca. (squam.) SW 900	52.1
astrocytoma SF-539	0.0	Lung ca. (squam.) NCI-H596	4.1
astrocytoma SNB-75	0.0	Mammary gland	11.8
glioma SNB-19	4.0	Breast ca.* (pl.ef) MCF-7	11.3
glioma U251	0.0	Breast ca.* (pl.ef) MDA-MB-231	1.4
glioma SF-295	2.8	Breast ca.* (pl. ef) T47D	6.3
Heart	13.9	Breast ca. BT-549	0.0
Skeletal Muscle	0.2	Breast ca. MDA-N	12.5
Bone marrow	0.7	Ovary	1.5
Thymus	0.0	Ovarian ca. OVCAR- 3	12.4
Spleen	0.7	Ovarian ca. OVCAR- 4	23.8
Lymph node	0.0	Ovarian ca. OVCAR- 5	38.2
Colorectal Tissue	4.5	Ovarian ca. OVCAR- 8	35.6
Stomach	2.6	Ovarian ca. IGROV- 1	2.4
Small intestine	2.6	Ovarian ca. (ascites) SK-OV-3	11.2
Colon ca. SW480	3.1	Uterus	1.7

Colon ca.* SW620 (SW480 met)	12.3	Placenta	0.8
Colon ca. HT29	12.3	Prostate	14.2
Colon ca. HCT-116	14.3	Prostate ca.* (bone met) PC-3	12.6
Colon ca. CaCo-2	11.5	Testis	0.4
Colon ca. Tissue (ODO3866)	5.7	Melanoma Hs688(A).T	6.5
Colon ca. HCC-2998	100.0	Melanoma* (met) Hs688(B).T	12.2
Gastric ca.* (liver met) NCI-N87	15.7	Melanoma UACC-62	0.0
Bladder	95.3	Melanoma M14	10.3
Trachea	1.0	Melanoma LOX IMVI	0.0
Kidney	55.9	Melanoma* (met) SK-MEL-5	0.0
Kidney (fetal)	7.7		

Table BHD. Panel 1.3D

Tissue Name	Rel. Exp.(%) Ag1519, Run 165529518	Tissue Name	Rel. Exp.(%) Ag1519, Run 165529518
Liver adenocarcinoma	0.0	Kidney (fetal)	0.0
Pancreas	38.7	Renal ca. 786-0	8.1
Pancreatic ca. CAPAN 2	7.9	Renal ca. A498	0.0
Adrenal gland	29.9	Renal ca. RXF 393	29.7
Thyroid	26.6	Renal ca. ACHN	13.4
Salivary gland	0.0	Renal ca. UO-31	0.0
Pituitary gland	17.2	Renal ca. TK-10	16.8
Brain (fetal)	0.0	Liver	0.0
Brain (whole)	0.0	Liver (fetal)	27.4
Brain (amygdala)	0.0	Liver ca. (hepatoblast) HepG2	0.0
Brain (cerebellum)	0.0	Lung	0.0
Brain (hippocampus)	0.0	Lung (fetal)	15.6
Brain (substantia nigra)	0.0	Lung ca. (small cell) LX-1	50.7
Brain (thalamus)	0.0	Lung ca. (small cell) NCI-H69	0.0
Cerebral Cortex	0.0	Lung ca. (s.cell var.) SHP-77	25.0
Spinal cord	0.0	Lung ca. (large	26.1

		cell)NCI-H460	
glio/astro U87-MG	0.0	Lung ca. (non-sm. cell) A549	0.0
glio/astro U-118-MG	0.0	Lung ca. (non-s.cell) NCI-H23	0.0
astrocytoma SW1783	0.0	Lung ca. (non-s.cell) HOP-62	27.4
neuro*; met SK-N-AS	0.0	Lung ca. (non-s.cl) NCI-H522	0.0
astrocytoma SF-539	0.0	Lung ca. (squam.) SW 900	18.0
astrocytoma SNB-75	0.0	Lung ca. (squam.) NCI-H596	0.0
glioma SNB-19	0.0	Mammary gland	27.0
glioma U251	18.8	Breast ca.* (pl.ef) MCF-7	27.0
glioma SF-295	0.0	Breast ca.* (pl.ef) MDA-MB-231	45.7
Heart (fetal)	16.4	Breast ca.* (pl.ef) T47D	13.7
Heart	0.0	Breast ca. BT-549	0.0
Skeletal muscle (fetal)	0.0	Breast ca. MDA-N	13.8
Skeletal muscle	18.8	Ovary	0.0
Bone marrow	0.0	Ovarian ca. OVCAR-3	0.0
Thymus	0.0	Ovarian ca. OVCAR-4	11.4
Spleen	0.0	Ovarian ca. OVCAR-5	2.6
Lymph node	34.4	Ovarian ca. OVCAR-8	12.3
Colorectal	100.0	Ovarian ca. IGROV-1	0.0
Stomach	0.0	Ovarian ca.* (ascites) SK-OV-3	33.7
Small intestine	0.0	Uterus	0.0
Colon ca. SW480	22.8	Placenta	17.6
Colon ca.* SW620(SW480 met)	10.0	Prostate	0.0
Colon ca. HT29	16.7	Prostate ca.* (bone met)PC-3	0.0
Colon ca. HCT-116	16.8	Testis	0.0
Colon ca. CaCo-2	15.6	Melanoma Hs688(A).T	15.1
Colon ca.	28.9	Melanoma* (met)	9.0

tissue(ODO3866)		Hs688(B).T	
Colon ca. HCC-2998	31.0	Melanoma UACC-62	0.0
Gastric ca.* (liver met) NCI-N87	36.6	Melanoma M14	26.2
Bladder	51.4	Melanoma LOX IMVI	0.0
Trachea	0.0	Melanoma* (met) SK-MEL-5	14.1
Kidney	56.3	Adipose	0.0

Table BHE. Panel 2D

Tissue Name	Rel. Exp.(%) Ag1519, Run 145158010	Tissue Name	Rel. Exp.(%) Ag1519, Run 145158010
Normal Colon	81.8	Kidney Margin 8120608	5.0
CC Well to Mod Diff (ODO3866)	6.0	Kidney Cancer 8120613	0.0
CC Margin (ODO3866)	7.3	Kidney Margin 8120614	1.9
CC Gr.2 rectosigmoid (ODO3868)	5.8	Kidney Cancer 9010320	7.6
CC Margin (ODO3868)	0.0	Kidney Margin 9010321	5.8
CC Mod Diff (ODO3920)	18.6	Normal Uterus	4.2
CC Margin (ODO3920)	10.6	Uterus Cancer 064011	47.3
CC Gr.2 ascend colon (ODO3921)	8.2	Normal Thyroid	21.6
CC Margin (ODO3921)	4.8	Thyroid Cancer 064010	42.3
CC from Partial Hepatectomy (ODO4309) Mets	47.6	Thyroid Cancer A302152	20.9
Liver Margin (ODO4309)	10.4	Thyroid Margin A302153	59.5
Colon mets to lung (OD04451-01)	12.2	Normal Breast	71.2
Lung Margin (OD04451- 02)	6.5	Breast Cancer (OD04566)	15.7
Normal Prostate 6546-1	11.6	Breast Cancer (OD04590-01)	19.9
Prostate Cancer (OD04410)	31.6	Breast Cancer Mets (OD04590-03)	41.5
Prostate Margin	25.5	Breast Cancer	33.7

(OD04410)		Metastasis (OD04655-05)	
Prostate Cancer (OD04720-01)	27.2	Breast Cancer 064006	27.0
Prostate Margin (OD04720-02)	31.4	Breast Cancer 1024	48.0
Normal Lung 061010	25.2	Breast Cancer 9100266	3.3
Lung Met to Muscle (ODO4286)	6.2	Breast Margin 9100265	7.8
Muscle Margin (ODO4286)	0.0	Breast Cancer A209073	24.8
Lung Malignant Cancer (OD03126)	39.0	Breast Margin A209073	32.3
Lung Margin (OD03126)	12.0	Normal Liver	3.5
Lung Cancer (OD04404)	4.9	Liver Cancer 064003	56.6
Lung Margin (OD04404)	27.9	Liver Cancer 1025	7.2
Lung Cancer (OD04565)	11.9	Liver Cancer 1026	1.8
Lung Margin (OD04565)	1.4	Liver Cancer 6004-T	6.0
Lung Cancer (OD04237- 01)	52.5	Liver Tissue 6004-N	0.0
Lung Margin (OD04237- 02)	20.7	Liver Cancer 6005-T	5.6
Ocular Mel Met to Liver (ODO4310)	5.6	Liver Tissue 6005-N	0.0
Liver Margin (ODO4310)	2.2	Normal Bladder	24.0
Melanoma Mets to Lung (OD04321)	0.0	Bladder Cancer 1023	3.3
Lung Margin (OD04321)	24.7	Bladder Cancer A302173	5.7
Normal Kidney	100.0	Bladder Cancer (OD04718-01)	2.9
Kidney Ca, Nuclear grade 2 (OD04338)	34.4	Bladder Normal Adjacent (OD04718- 03)	0.0
Kidney Margin (OD04338)	54.7	Normal Ovary	3.9
Kidney Ca Nuclear grade 1/2 (OD04339)	81.8	Ovarian Cancer 064008	7.2
Kidney Margin (OD04339)	48.3	Ovarian Cancer (OD04768-07)	38.4
Kidney Ca, Clear cell type (OD04340)	11.0	Ovary Margin (OD04768-08)	5.1
Kidney Margin (OD04340)	56.6	Normal Stomach	11.4

Kidney Ca, Nuclear grade 3 (OD04348)	3.4	Gastric Cancer 9060358	6.5
Kidney Margin (OD04348)	43.2	Stomach Margin 9060359	0.0
Kidney Cancer (OD04622-01)	11.5	Gastric Cancer 9060395	6.7
Kidney Margin (OD04622-03)	3.5	Stomach Margin 9060394	4.5
Kidney Cancer (OD04450-01)	17.8	Gastric Cancer 9060397	0.0
Kidney Margin (OD04450-03)	42.0	Stomach Margin 9060396	6.7
Kidney Cancer 8120607	0.0	Gastric Cancer 064005	16.6

CNS_neurodegeneration_v1.0 Summary: Ag3460 Expression of the CG59540-01 gene is low/undetectable (CT values > 35) across the samples in this panel.

General_screening_panel_v1.4 Summary: Ag3460 Expression of the CG59540-01 gene is low/undetectable (CT values > 35) across the samples in this panel.

Panel 1.2 Summary: Ag1519 The expression of the CG59540-01 gene appears to be highest in a sample derived from a colon cancer cell line (HCC-2998) (CT=28.2). In addition, there is substantial expression associated with normal kidney and bladder. Thus, the expression of this gene could be used to distinguish these tissues from other tissues in the panel. In addition there was noted expression clustered in ovarian, renal and colon cancer cell lines. Therefore, therapeutic modulation of this gene, through the use of small molecule drugs, antibodies or protein therapeutics might be of use in the treatment of colon cancer, renal cancer or ovarian cancer.

Among tissues with metabolic function, there is moderate expression in fetal and adult heart, adrenal, and pancreas. This expression suggests that therapeutic modulation of the expression or function of the protein encoded by this gene may be useful in the treatment of diseases that involve these tissues, including obesity and diabetes.

In addition, there appears to be higher levels of expression in adult heart (CT=31) when compared to expression in fetal heart (CT=34.4). Thus, expression of this gene could be used to differentiate between adult and fetal heart tissue. Conversely, expression of this gene is

higher in fetal lung (CT=34.5) than in adult lung (CT=40). Thus, expression of this gene could also be used to differentiate between adult and fetal lung.

Panel 1.3D Summary: Ag1519 Significant expression the CG59540-01 gene is limited to a sample derived from colorectal tissue (CT=34.3). Thus, expression of this gene could be used to differentiate between this sample and other samples on this panel, and between colorectal tissue and other normal or malignant tissues.

Panel 2D Summary: Ag1519 The expression of the CG59540-01 gene in panel 2 appears to be highest in a samples derived from normal kidney tissue (CT=32). In addition there appears to be substantial difference in expression between normal kidney adjacent to cancer tissue and the cancer tissue itself. Thus, the expression of this gene could be used to distinguish normal kidney tissue from other samples in the panel. In addition, the expression of this gene could be used to distinguish normal kidney from malignant tissue. Moreover, therapeutic modulation of this gene, through the use of small molecule drugs, antibodies or protein therapeutics might be of use in the treatment of kidney cancer.

Panel 4D Summary: Ag3460 Expression of the CG59540-01 gene is low/undetectable (CT values > 35) across the samples in this panel.

BI. CG59280-01 and CG59280-02: OLFACTORY RECEPTOR

Expression of gene CG59280-01 and CG59280-02 was assessed using the primer-probe set Ag3527, described in Table BIA. Results of the RTQ-PCR runs are shown in Table BIB. Please note that CG59280-02 represents a full-length physical clone of the CG59280-01 gene, validating the prediction of the gene sequence.

Table BIA. Probe Name Ag3527

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-atggccattgataggtacgtt-3'	21	361	580
Probe	TET-5'-catctgtaaccctctccgctacccaa-3'-TAMRA	26	384	581
Reverse	5'-ccacagagagctgaacacaga-3'	21	428	582

Table BIB. Panel 4D

Tissue Name	Rel. Exp.(%)	Tissue Name	Rel. Exp.(%)
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	Ag3527, Run 166446354		Ag3527, Run 166446354
Secondary Th1 act	0.0	HUVEC IL-1beta	0.0
Secondary Th2 act	0.0	HUVEC IFN gamma	0.0
Secondary Tr1 act	0.0	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	0.0	HUVEC IL-11	0.0
Secondary Tr1 rest	2.0	Lung Microvascular EC none	0.0
Primary Th1 act	0.0	Lung Microvascular EC TNFalpha + IL-1beta	0.0
Primary Th2 act	0.0	Microvascular Dermal EC none	4.2
Primary Tr1 act	0.0	Microvascular Dermal EC TNFalpha + IL-1beta	0.0
Primary Th1 rest	0.0	Bronchial epithelium TNFalpha + IL1beta	4.2
Primary Th2 rest	0.0	Small airway epithelium none	0.0
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	0.0
CD45RA CD4 lymphocyte act	0.0	Coronary artery SMC rest	0.0
CD45RO CD4 lymphocyte act	0.0	Coronary artery SMC TNFalpha + IL-1beta	0.0
CD8 lymphocyte act	0.0	Astrocytes rest	0.0
Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFalpha + IL-1beta	0.0
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	4.4	KU-812 (Basophil) PMA/ionomycin	0.0
2ry Th1/Th2/Tr1_anti- CD95 CH11	0.0	CCD1106 (Keratinocytes) none	0.0
LAK cells rest	0.0	CCD1106 (Keratinocytes) TNFalpha + IL 1beta	0.0
LAK cells IL-2	0.0	Liver cirrhosis	100.0
LAK cells IL-2+IL-12	0.0	Lupus kidney	0.0
LAK cells IL-2+IFN gamma	5.1	NCI-H292 none	0.0
LAK cells IL-2+ IL-18	0.0	NCI-H292 IL-4	0.0
LAK cells PMA/ionomycin	0.0	NCI-H292 IL-9	0.0
NK Cells IL-2 rest	0.0	NCI-H292 IL-13	0.0

Two Way MLR 3 day	0.0	NCI-H292 IFN gamma	0.0
Two Way MLR 5 day	0.0	HPAEC none	4.5
Two Way MLR 7 day	0.0	HPAEC TNF alpha + IL-1 beta	0.0
PBMC rest	3.1	Lung fibroblast none	0.0
PBMC PWM	0.0	Lung fibroblast TNF alpha + IL-1 beta	0.0
PBMC PHA-L	0.0	Lung fibroblast IL-4	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-9	0.0
Ramos (B cell) ionomycin	0.0	Lung fibroblast IL-13	0.0
B lymphocytes PWM	0.0	Lung fibroblast IFN gamma	0.0
B lymphocytes CD40L and IL-4	0.0	Dermal fibroblast CCD1070 rest	0.0
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 TNF alpha	0.0
EOL-1 dbcAMP PMA/ionomycin	0.0	Dermal fibroblast CCD1070 IL-1 beta	0.0
Dendritic cells none	4.5	Dermal fibroblast IFN gamma	0.0
Dendritic cells LPS	5.3	Dermal fibroblast IL-4	0.0
Dendritic cells anti-CD40	9.9	IBD Colitis 2	10.8
Monocytes rest	0.0	IBD Crohn's	8.9
Monocytes LPS	27.0	Colon	0.0
Macrophages rest	9.5	Lung	4.6
Macrophages LPS	4.0	Thymus	0.0
HUVEC none	0.0	Kidney	0.0
HUVEC starved	0.0		

CNS_neurodegeneration_v1.0 Summary: Ag3527 Expression of the CG59280-01 gene is low/undetectable (CT values > 35) across the samples in this panel. (Data not shown.)

General_screening_panel_v1.4 Summary: Ag3527 Expression of the CG59280-01 gene is low/undetectable (CT values > 35) across the samples in this panel. (Data not shown.) This gene encodes a G protein-coupled receptor (GPCR), a type of cell surface receptor involved in signal transduction. It is most similar to members of the odorant receptor subfamily of GPCRs. Based on analogy to other odorant receptor genes, we predict that expression of this gene may be highest in nasal epithelium, a sample not represented on this panel.

Panel 4D Summary: Ag3527 Highest expression of the CG59280-01 gene is seen in the liver cirrhosis sample(CT=31.81). Thus, expression of this gene could be used to differentiate between this sample from the other samples on this panel and as a marker to detect the presence of liver cirrhosis. Furthermore, expression of this gene is not detected in normal liver in Panel 1.4, suggesting that its expression is unique to liver cirrhosis. This gene encodes a putative GPCR; therefore, antibodies or small molecule therapeutics could reduce or inhibit fibrosis that occurs in liver cirrhosis. In addition, antibodies to this putative GPCR could also be used for the diagnosis of liver cirrhosis.

BJ. CG59568-01: GPCR

Expression of gene CG59568-01 was assessed using the primer-probe set Ag3474, described in Table BJA. Results of the RTQ-PCR runs are shown in Table BJB.

Table BJA. Probe Name Ag3474

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-ttacagcaatcaccatgggtctt-3'	22	475	760
Probe	TET-5'-accttctgtggacctatgaaactga-3'- TAMRA	26	510	761
Reverse	5'-gggtgaagtcacaaaagaagtg-3'	22	537	762

Table BJB. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3474, Run 166417193	Tissue Name	Rel. Exp.(%) Ag3474, Run 166417193
Secondary Th1 act	7.1	HUVEC IL-1beta	0.0
Secondary Th2 act	0.0	HUVEC IFN gamma	0.0
Secondary Tr1 act	4.2	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	0.0	HUVEC IL-11	0.0
Secondary Tr1 rest	0.0	Lung Microvascular EC none	0.0
Primary Th1 act	0.0	Lung Microvascular EC TNFalpha + IL-1beta	0.0
Primary Th2 act	2.2	Microvascular Dermal EC none	0.0

Primary Tr1 act	0.0	Microsvascular Dermal EC TNFalpha + IL-1beta	0.0
Primary Th1 rest	3.3	Bronchial epithelium TNFalpha + IL1beta	0.0
Primary Th2 rest	5.9	Small airway epithelium none	0.0
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	0.3
CD45RA CD4 lymphocyte act	0.0	Coronary artery SMC rest	0.0
CD45RO CD4 lymphocyte act	0.0	Coronary artery SMC TNFalpha + IL-1beta	0.0
CD8 lymphocyte act	0.0	Astrocytes rest	0.0
Secondary CD8 lymphocyte rest	1.7	Astrocytes TNFalpha + IL-1beta	0.0
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	3.1
2ry Th1/Th2/Tr1_anti- CD95 CH11	0.0	CCD1106 (Keratinocytes) none	0.0
LAK cells rest	0.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.5
LAK cells IL-2	0.0	Liver cirrhosis	100.0
LAK cells IL-2+IL-12	3.6	Lupus kidney	0.0
LAK cells IL-2+IFN gamma	3.9	NCI-H292 none	0.0
LAK cells IL-2+ IL-18	2.4	NCI-H292 IL-4	0.0
LAK cells PMA/ionomycin	0.0	NCI-H292 IL-9	0.0
NK Cells IL-2 rest	0.0	NCI-H292 IL-13	0.0
Two Way MLR 3 day	0.0	NCI-H292 IFN gamma	0.0
Two Way MLR 5 day	0.0	HPAEC none	0.0
Two Way MLR 7 day	0.0	HPAEC TNF alpha + IL-1 beta	0.0
PBMC rest	0.0	Lung fibroblast none	0.0
PBMC PWM	0.0	Lung fibroblast TNF alpha + IL-1 beta	6.2
PBMC PHA-L	0.0	Lung fibroblast IL-4	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-9	0.0
Ramos (B cell) ionomycin	0.0	Lung fibroblast IL-13	0.3
B lymphocytes PWM	8.4	Lung fibroblast IFN gamma	0.0
B lymphocytes CD40L	0.0	Dermal fibroblast	0.0

and IL-4		CCD1070 rest	
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 TNF alpha	1.6
EOL-1 dbcAMP PMA/ionomycin	0.0	Dermal fibroblast CCD1070 IL-1 beta	0.0
Dendritic cells none	0.0	Dermal fibroblast IFN gamma	0.0
Dendritic cells LPS	1.5	Dermal fibroblast IL-4	0.0
Dendritic cells anti- CD40	0.0	IBD Colitis 2	11.9
Monocytes rest	0.0	IBD Crohn's	0.0
Monocytes LPS	5.8	Colon	1.5
Macrophages rest	3.4	Lung	0.0
Macrophages LPS	0.0	Thymus	3.8
HUVEC none	0.0	Kidney	6.7
HUVEC starved	0.0		

CNS_neurodegeneration_v1.0 Summary: Ag3474 Expression of the CG59568-01 gene is low/undetectable (CT values > 35) across the samples in this panel. (Data not shown.)

General_screening_panel_v1.4 Summary: Ag3474 Expression of the CG59568-01 gene is low/undetectable (CT values > 35) across the samples in this panel. (Data not shown.) This gene encodes a G protein-coupled receptor (GPCR), a type of cell surface receptor involved in signal transduction. It is most similar to members of the odorant receptor subfamily of GPCRs. Based on analogy to other odorant receptor genes, we predict that expression of this gene may be highest in nasal epithelium, a sample not represented on this panel.

Panel 4D Summary: Ag3474 Highest expression of the CG59280-01 gene is seen in the liver cirrhosis sample(CT=31.37). Thus, expression of this gene could be used to differentiate between this sample from the other samples on this panel and as a marker to detect the presence of liver cirrhosis. Furthermore, expression of this gene is not detected in normal liver in Panel 1.4, suggesting that its expression is unique to liver cirrhosis. This gene encodes a putative GPCR; therefore, antibodies or small molecule therapeutics could reduce or inhibit fibrosis that occurs in liver cirrhosis. In addition, antibodies to this putative GPCR could also be used for the diagnosis of liver cirrhosis.

References:

1. Mark M.D., Wittemann S., Herlitz S. (2000) G protein modulation of recombinant P/Q-type calcium channels by regulators of G protein signalling proteins. J. Physiol. 528 Pt 1: 65-77.

BK. CG59224-01 and CG59216-01: GPCR

Expression of gene CG59224-01 and variant CG59216-01 was assessed using the primer-probe sets Ag3400 and Ag3405, described in Tables BKA and BKB. Results of the RTQ-PCR runs are shown in Table BKC.

Table BKA. Probe Name Ag3400

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-tctctgacctagggtgtctct-3'	22	225	584
Probe	TET-5'-tcttccttaccatcactttgggact-3'-TAMRA	26	248	585
Reverse	5'-catgaatttcatggacatcaaa-3'	22	281	586

Table BKB. Probe Name Ag3405

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-cacatctgtgctgtgcttatct-3'	22	746	587
Probe	TET-5'-agtgtgcatgctccaccagttt-3'-TAMRA	24	785	588
Reverse	5'-acgtggatcataggagacacat-3'	22	816	589

Table BKC. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3400, Run 216822602	Rel. Exp.(%) Ag3405, Run 216838741	Tissue Name	Rel. Exp.(%) Ag3400, Run 216822602	Rel. Exp.(%) Ag3405, Run 216838741
Adipose	0.0	0.0	Renal ca. TK-10	0.0	0.0
Melanoma* Hs688(A).T	0.0	0.0	Bladder	1.2	0.0
Melanoma* Hs688(B).T	0.0	0.0	Gastric ca. (liver met.) NCI-N87	0.0	0.0
Melanoma* M14	0.0	0.0	Gastric ca. KATO III	0.0	0.0
Melanoma* LOXIMVI	0.0	0.0	Colon ca. SW- 948	0.0	0.0
Melanoma* SK-MEL-5	0.0	0.0	Colon ca. SW480	0.0	0.0

Squamous cell carcinoma SCC-4	0.0	0.0	Colon ca.* (SW480 met) SW620	0.0	0.0
Testis Pool	0.0	0.0	Colon ca. HT29	0.0	0.0
Prostate ca.* (bone met) PC-3	0.0	0.0	Colon ca. HCT-116	0.0	0.0
Prostate Pool	3.2	1.8	Colon ca. CaCo-2	0.0	0.0
Placenta	0.0	0.0	Colon cancer tissue	0.0	0.0
Uterus Pool	0.0	0.0	Colon ca. SW1116	0.0	0.0
Ovarian ca. OVCAR-3	0.0	0.0	Colon ca. Colo-205	0.0	0.0
Ovarian ca. SK-OV-3	1.0	0.0	Colon ca. SW-48	0.0	0.0
Ovarian ca. OVCAR-4	0.0	0.0	Colon Pool	0.0	0.0
Ovarian ca. OVCAR-5	0.0	0.0	Small Intestine Pool	0.0	0.0
Ovarian ca. IGROV-1	0.0	0.0	Stomach Pool	0.0	0.0
Ovarian ca. OVCAR-8	0.0	0.0	Bone Marrow Pool	0.0	0.0
Ovary	0.0	0.0	Fetal Heart	0.0	0.0
Breast ca. MCF-7	0.0	0.0	Heart Pool	1.7	1.3
Breast ca. MDA-MB-231	0.0	0.0	Lymph Node Pool	0.0	0.0
Breast ca. BT 549	0.0	0.0	Fetal Skeletal Muscle	0.0	0.0
Breast ca. T47D	0.0	0.0	Skeletal Muscle Pool	0.0	0.0
Breast ca. MDA-N	0.0	0.5	Spleen Pool	0.0	0.0
Breast Pool	0.0	0.5	Thymus Pool	0.0	0.5
Trachea	0.0	0.0	CNS cancer (glio/astro) U87-MG	0.0	0.0
Lung	0.0	0.0	CNS cancer (glio/astro) U-118-MG	0.0	0.0
Fetal Lung	0.0	0.0	CNS cancer (neuro;met) SK-N-AS	0.0	0.0

Lung ca. NCI-N417	0.0	0.0	CNS cancer (astro) SF-539	0.0	0.0
Lung ca. LX-1	0.0	0.0	CNS cancer (astro) SNB-75	0.0	0.0
Lung ca. NCI-H146	2.5	3.3	CNS cancer (glio) SNB-19	0.0	0.0
Lung ca. SHP-77	100.0	100.0	CNS cancer (glio) SF-295	0.0	0.0
Lung ca. A549	0.0	0.0	Brain (Amygdala) Pool	0.0	0.0
Lung ca. NCI-H526	0.0	0.0	Brain (cerebellum)	0.0	0.0
Lung ca. NCI-H23	0.0	0.0	Brain (fetal)	0.0	0.0
Lung ca. NCI-H460	0.0	0.0	Brain (Hippocampus) Pool	0.0	0.0
Lung ca. HOP-62	0.0	0.0	Cerebral Cortex Pool	0.0	0.6
Lung ca. NCI-H522	0.0	0.0	Brain (Substantia nigra) Pool	0.0	0.0
Liver	0.0	0.0	Brain (Thalamus) Pool	0.0	0.0
Fetal Liver	0.0	0.0	Brain (whole)	0.0	0.0
Liver ca. HepG2	0.0	0.0	Spinal Cord Pool	0.0	0.0
Kidney Pool	0.0	0.4	Adrenal Gland	0.0	0.0
Fetal Kidney	10.8	2.6	Pituitary gland Pool	0.0	0.0
Renal ca. 786-0	0.0	0.0	Salivary Gland	0.0	0.0
Renal ca. A498	0.0	0.0	Thyroid (female)	0.0	0.0
Renal ca. ACHN	0.0	0.0	Pancreatic ca. CAPAN2	0.0	0.0
Renal ca. UO-31	0.0	0.0	Pancreas Pool	0.0	1.2

CNS_neurodegeneration_v1.0 Summary: Ag3400/Ag3405 Expression of the CG59224-01 gene is low/undetectable (CT values > 35) across the samples in this panel. (Data not shown.)

General_screening_panel_v1.4 Summary: Ag3400/Ag3405 Two experiments with two different probe and primer sets produce results that are in excellent agreement, with significant expression of the CG59224-01 gene exclusively in a lung cancer cell line sample (CTs = 30-

33). Therefore, expression of this gene may be used to distinguish this sample from other samples on this panel and as a marker for lung cancer. Furthermore, therapeutic modulation of the activity of the GPCR encoded by this gene may be beneficial in the treatment of lung cancer.

Panel 4D Summary: Ag3400/Ag3405 Expression of the CG59224-01 gene is low/undetectable (CT values > 35) across the samples in this panel. (Data not shown.) This gene encodes a G protein-coupled receptor (GPCR), a type of cell surface receptor involved in signal transduction. It is most similar to members of the odorant receptor subfamily of GPCRs. Based on analogy to other odorant receptor genes, we predict that expression of this gene may be highest in nasal epithelium, a sample not represented on this panel.

BL. CG59214-01 and CG59214-01: GPCR

Expression of gene CG59214-01 and CG59214-01 was assessed using the primer-probe sets Ag3398 and Ag3404, described in Tables BLA and BLB. Results of the RTQ-PCR runs are shown in Tables BLC and BLD.

Table BLA. Probe Name Ag3398

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-atacttgcacatctccacacatctg-3'	22	724	590
Probe	TET-5'-caccaatgattgggctatctatgatcca-3'-TAMRA	28	766	591
Reverse	5'-tgaggaagcattctgtccatag-3'	22	797	592

Table BLB. Probe Name Ag3404

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-atacttgcacatctccacacatctg-3'	22	724	593
Probe	TET-5'-caccaatgattgggctatctatgatcca-3'-TAMRA	28	766	594
Reverse	5'-tgaggaagcattctgtccatag-3'	22	797	595

Table BLC. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3398, Run 216822567	Rel. Exp.(%) Ag3404, Run 216838380	Tissue Name	Rel. Exp.(%) Ag3398, Run 216822567	Rel. Exp.(%) Ag3404, Run 216838380
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Adipose	0.0	0.0	Renal ca. TK-10	0.0	0.0
Melanoma* Hs688(A).T	0.0	0.0	Bladder	0.0	0.0
Melanoma* Hs688(B).T	0.0	0.0	Gastric ca. (liver met.) NCI-N87	0.0	0.0
Melanoma* M14	0.0	0.0	Gastric ca. KATO III	0.0	0.0
Melanoma* LOXIMV1	0.0	0.0	Colon ca. SW- 948	0.0	0.0
Melanoma* SK-MEL-5	0.0	88.9	Colon ca. SW480	0.0	0.0
Squamous cell carcinoma SCC-4	0.0	0.0	Colon ca.* (SW480 met) SW620	0.0	0.0
Testis Pool	0.0	0.0	Colon ca. HT29	0.0	0.0
Prostate ca.* (bone met) PC-3	0.0	0.0	Colon ca. HCT- 116	0.0	0.0
Prostate Pool	0.0	0.0	Colon ca. CaCo-2	0.0	0.0
Placenta	0.0	0.0	Colon cancer tissue	0.0	0.0
Uterus Pool	0.0	0.0	Colon ca. SW1116	0.0	0.0
Ovarian ca. OVCAR-3	0.0	0.0	Colon ca. Colo- 205	0.0	0.0
Ovarian ca. SK-OV-3	0.0	0.0	Colon ca. SW-48	0.0	0.0
Ovarian ca. OVCAR-4	0.0	0.0	Colon Pool	0.0	0.0
Ovarian ca. OVCAR-5	0.0	0.0	Small Intestine Pool	0.0	8.9
Ovarian ca. IGROV-1	0.0	0.0	Stomach Pool	0.0	15.6
Ovarian ca. OVCAR-8	0.0	0.0	Bone Marrow Pool	0.0	0.0
Ovary	0.0	7.5	Fetal Heart	0.0	0.0
Breast ca. MCF-7	0.0	0.0	Heart Pool	0.0	0.0
Breast ca. MDA-MB- 231	0.0	0.0	Lymph Node Pool	0.0	0.0
Breast ca. BT 549	0.0	0.0	Fetal Skeletal Muscle	0.0	0.0
Breast ca. T47D	0.0	0.0	Skeletal Muscle Pool	0.0	0.0

Breast ca. MDA-N	6.9	0.0	Spleen Pool	0.0	0.0
Breast Pool	0.0	0.0	Thymus Pool	0.0	0.0
Trachea	0.0	0.0	CNS cancer (glio/astro) U87-MG	0.0	0.0
Lung	0.0	0.0	CNS cancer (glio/astro) U-118-MG	0.0	12.5
Fetal Lung	0.0	0.0	CNS cancer (neuro;met) SK-N-AS	0.0	0.0
Lung ca. NCI-N417	0.0	0.0	CNS cancer (astro) SF-539	0.0	0.0
Lung ca. LX-1	0.0	0.0	CNS cancer (astro) SNB-75	0.0	0.0
Lung ca. NCI-H146	0.0	0.0	CNS cancer (glio) SNB-19	0.0	0.0
Lung ca. SHP-77	100.0	100.0	CNS cancer (glio) SF-295	0.0	0.0
Lung ca. A549	0.0	0.0	Brain (Amygdala) Pool	0.0	0.0
Lung ca. NCI-H526	0.0	0.0	Brain (cerebellum)	0.0	0.0
Lung ca. NCI-H23	0.0	0.0	Brain (fetal)	0.0	0.0
Lung ca. NCI-H460	0.0	0.0	Brain (Hippocampus) Pool	0.0	0.0
Lung ca. HOP-62	0.0	0.0	Cerebral Cortex Pool	0.0	0.0
Lung ca. NCI-H522	0.0	0.0	Brain (Substantia nigra) Pool	0.0	0.0
Liver	0.0	0.0	Brain (Thalamus) Pool	4.3	0.0
Fetal Liver	0.0	0.0	Brain (whole)	0.0	0.0
Liver ca. HepG2	0.0	0.0	Spinal Cord Pool	0.0	0.0
Kidney Pool	0.0	0.0	Adrenal Gland	0.0	0.0
Fetal Kidney	11.1	8.5	Pituitary gland Pool	0.0	0.0
Renal ca. 786-0	0.0	0.0	Salivary Gland	0.0	0.0
Renal ca. A498	0.0	0.0	Thyroid (female)	0.0	0.0
Renal ca.	0.0	0.0	Pancreatic ca.	0.0	0.0

ACHN			CAPAN2		
Renal ca. UO-31	0.0	0.0	Pancreas Pool	0.0	0.0

Table BLD. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3404, Run 165825947	Tissue Name	Rel. Exp.(%) Ag3404, Run 165825947
Secondary Th1 act	0.0	HUVEC IL-1beta	0.0
Secondary Th2 act	0.0	HUVEC IFN gamma	0.0
Secondary Tr1 act	0.0	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	0.0	HUVEC IL-11	0.0
Secondary Tr1 rest	0.0	Lung Microvascular EC none	0.0
Primary Th1 act	0.0	Lung Microvascular EC TNFalpha + IL-1beta	0.0
Primary Th2 act	0.0	Microvascular Dermal EC none	0.0
Primary Tr1 act	0.0	Microvascular Dermal EC TNFalpha + IL-1beta	0.0
Primary Th1 rest	0.0	Bronchial epithelium TNFalpha + IL1beta	0.0
Primary Th2 rest	0.0	Small airway epithelium none	0.0
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	0.0
CD45RA CD4 lymphocyte act	0.0	Coronary artery SMC rest	0.0
CD45RO CD4 lymphocyte act	0.0	Coronary artery SMC TNFalpha + IL-1beta	0.0
CD8 lymphocyte act	0.0	Astrocytes rest	0.0
Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFalpha + IL-1beta	0.0
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	5.8
2ry Th1/Th2/Tr1_anti-CD95 CH11	8.9	CCD1106 (Keratinocytes) none	0.0
LAK cells rest	0.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0
LAK cells IL-2	0.0	Liver cirrhosis	100.0

LAK cells IL-2+IL-12	0.0	Lupus kidney	0.0
LAK cells IL-2+IFN gamma	0.0	NCI-H292 none	0.0
LAK cells IL-2+ IL-18	0.0	NCI-H292 IL-4	0.0
LAK cells PMA/ionomycin	0.0	NCI-H292 IL-9	0.0
NK Cells IL-2 rest	0.0	NCI-H292 IL-13	0.0
Two Way MLR 3 day	0.0	NCI-H292 IFN gamma	0.0
Two Way MLR 5 day	0.0	HPAEC none	0.0
Two Way MLR 7 day	0.0	HPAEC TNF alpha + IL-1 beta	0.0
PBMC rest	0.0	Lung fibroblast none	0.0
PBMC PWM	0.0	Lung fibroblast TNF alpha + IL-1 beta	0.0
PBMC PHA-L	0.0	Lung fibroblast IL-4	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-9	0.0
Ramos (B cell) ionomycin	0.0	Lung fibroblast IL-13	0.0
B lymphocytes PWM	0.0	Lung fibroblast IFN gamma	0.0
B lymphocytes CD40L and IL-4	0.0	Dermal fibroblast CCD1070 rest	0.0
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 TNF alpha	0.0
EOL-1 dbcAMP PMA/ionomycin	0.0	Dermal fibroblast CCD1070 IL-1 beta	0.0
Dendritic cells none	0.0	Dermal fibroblast IFN gamma	0.0
Dendritic cells LPS	0.0	Dermal fibroblast IL-4	3.9
Dendritic cells anti-CD40	0.0	IBD Colitis 2	7.2
Monocytes rest	0.0	IBD Crohn's	4.0
Monocytes LPS	0.0	Colon	5.5
Macrophages rest	0.0	Lung	3.1
Macrophages LPS	0.0	Thymus	0.0
HUVEC none	0.0	Kidney	0.0
HUVEC starved	0.0		

CNS_neurodegeneration_v1.0 Summary: Ag3398/Ag3404 Expression of the CG59222-01 gene is low/undetectable (CT values > 35) across the samples in this panel. (Data not shown.)

General_screening_panel_v1.4 Summary: Ag3398/Ag3404 Two experiments with two different probe and primer sets produce results that are in excellent agreement, with significant

expression of the CG59222-01 gene exclusively in a lung cancer cell line sample (CT = 33.8). Therefore, expression of this gene may be used to this sample from other samples on this panel and as a marker for lung cancer. Furthermore, therapeutic modulation of the activity of the GPCR encoded by this gene may be beneficial in the treatment of lung cancer.

Panel 4D Summary: Ag3404 Highest expression of the CG59222-01 gene is seen in the liver cirrhosis sample (CT=32.65). Thus, expression of this gene could be used to differentiate between this sample from the other samples on this panel and as a marker to detect the presence of liver cirrhosis. Furthermore, expression of this gene is not detected in normal liver in Panel 1.4, suggesting that its expression is unique to liver cirrhosis. This gene encodes a putative GPCR; therefore, antibodies or small molecule therapeutics could reduce or inhibit fibrosis that occurs in liver cirrhosis. In addition, antibodies to this putative GPCR could also be used for the diagnosis of liver cirrhosis. Ag3398 Expression of CG59222-01 gene is low/undetectable (CTs > 35) across all of the samples on this panel (Data not shown).

BM. CG59220-01: GPCR

Expression of gene CG59220-01 was assessed using the primer-probe set Ag3402, described in Table BMA. Results of the RTQ-PCR runs are shown in Tables BMB, BMC and BMD.

Table BMA. Probe Name Ag3402

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-ctccacacacccatgtacttct-3'	22	160	596
Probe	TET-5'-cttgatctctgccattcctctgtca-3'- TAMRA	26	201	597
Reverse	5'-aggaggttctccaacagcttag-3'	22	233	598

Table BMB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3402, Run 210349784	Tissue Name	Rel. Exp.(%) Ag3402, Run 210349784
AD 1 Hippo	9.0	Control (Path) 3 Temporal Ctx	18.6
AD 2 Hippo	46.3	Control (Path) 4 Temporal Ctx	56.6
AD 3 Hippo	8.8	AD 1 Occipital Ctx	21.6
AD 4 Hippo	24.1	AD 2 Occipital Ctx	0.0

		(Missing)	
AD 5 Hippo	52.9	AD 3 Occipital Ctx	15.0
AD 6 Hippo	39.2	AD 4 Occipital Ctx	48.0
Control 2 Hippo	41.8	AD 5 Occipital Ctx	56.3
Control 4 Hippo	18.2	AD 6 Occipital Ctx	31.4
Control (Path) 3 Hippo	13.7	Control 1 Occipital Ctx	14.4
AD 1 Temporal Ctx	27.4	Control 2 Occipital Ctx	55.5
AD 2 Temporal Ctx	57.0	Control 3 Occipital Ctx	42.3
AD 3 Temporal Ctx	10.2	Control 4 Occipital Ctx	21.2
AD 4 Temporal Ctx	54.3	Control (Path) 1 Occipital Ctx	100.0
AD 5 Inf Temporal Ctx	42.9	Control (Path) 2 Occipital Ctx	27.7
AD 5 Sup Temporal Ctx	28.7	Control (Path) 3 Occipital Ctx	9.0
AD 6 Inf Temporal Ctx	41.8	Control (Path) 4 Occipital Ctx	34.2
AD 6 Sup Temporal Ctx	51.4	Control 1 Parietal Ctx	23.5
Control 1 Temporal Ctx	18.2	Control 2 Parietal Ctx	28.5
Control 2 Temporal Ctx	43.2	Control 3 Parietal Ctx	29.5
Control 3 Temporal Ctx	32.8	Control (Path) 1 Parietal Ctx	99.3
Control 3 Temporal Ctx	20.0	Control (Path) 2 Parietal Ctx	46.7
Control (Path) 1 Temporal Ctx	87.1	Control (Path) 3 Parietal Ctx	12.0
Control (Path) 2 Temporal Ctx	60.3	Control (Path) 4 Parietal Ctx	82.4

Table BMC. General screening panel v1.4

Tissue Name	Rel. Exp.(%) Ag3402, Run 216823314	Tissue Name	Rel. Exp.(%) Ag3402, Run 216823314
Adipose	14.7	Renal ca. TK-10	2.5
Melanoma* Hs688(A).T	10.1	Bladder	28.7
Melanoma* Hs688(B).T	1.4	Gastric ca. (liver met.) NCI-N87	17.9

Melanoma* M14	0.9	Gastric ca. KATO III	0.7
Melanoma* LOXIMVI	0.8	Colon ca. SW-948	0.0
Melanoma* SK- MEL-5	2.1	Colon ca. SW480	1.7
Squamous cell carcinoma SCC-4	2.9	Colon ca.* (SW480 met) SW620	1.8
Testis Pool	25.9	Colon ca. HT29	1.3
Prostate ca.* (bone met) PC-3	1.2	Colon ca. HCT-116	0.0
Prostate Pool	16.0	Colon ca. CaCo-2	0.7
Placenta	1.3	Colon cancer tissue	7.4
Uterus Pool	15.6	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	3.1	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV- 3	6.0	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	0.6	Colon Pool	49.7
Ovarian ca. OVCAR-5	2.9	Small Intestine Pool	53.6
Ovarian ca. IGROV- 1	1.6	Stomach Pool	15.8
Ovarian ca. OVCAR-8	1.6	Bone Marrow Pool	14.5
Ovary	48.3	Fetal Heart	9.1
Breast ca. MCF-7	0.6	Heart Pool	39.5
Breast ca. MDA- MB-231	0.0	Lymph Node Pool	39.2
Breast ca. BT 549	2.4	Fetal Skeletal Muscle	5.8
Breast ca. T47D	1.3	Skeletal Muscle Pool	47.6
Breast ca. MDA-N	0.4	Spleen Pool	22.2
Breast Pool	31.6	Thymus Pool	12.9
Trachea	5.9	CNS cancer (glio/astro) U87-MG	0.8
Lung	16.6	CNS cancer (glio/astro) U-118-MG	3.4
Fetal Lung	30.8	CNS cancer (neuro;met) SK-N-AS	1.5
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF- 539	0.0
Lung ca. LX-1	9.7	CNS cancer (astro) SNB-75	1.1
Lung ca. NCI-H146	0.0	CNS cancer (glio) SNB-19	1.1

Lung ca. SHP-77	0.6	CNS cancer (glio) SF-295	4.1
Lung ca. A549	0.6	Brain (Amygdala) Pool	28.1
Lung ca. NCI-H526	0.0	Brain (cerebellum)	35.1
Lung ca. NCI-H23	5.9	Brain (fetal)	12.3
Lung ca. NCI-H460	0.9	Brain (Hippocampus) Pool	39.8
Lung ca. HOP-62	1.6	Cerebral Cortex Pool	88.9
Lung ca. NCI-H522	7.1	Brain (Substantia nigra) Pool	43.2
Liver	0.0	Brain (Thalamus) Pool	74.2
Fetal Liver	2.5	Brain (whole)	26.1
Liver ca. HepG2	0.7	Spinal Cord Pool	100.0
Kidney Pool	51.8	Adrenal Gland	24.1
Fetal Kidney	16.7	Pituitary gland Pool	8.6
Renal ca. 786-0	0.8	Salivary Gland	3.2
Renal ca. A498	0.0	Thyroid (female)	8.9
Renal ca. ACHN	1.4	Pancreatic ca. CAPAN2	0.8
Renal ca. UO-31	1.5	Pancreas Pool	24.8

Table BMD. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3402, Run 165825209	Tissue Name	Rel. Exp.(%) Ag3402, Run 165825209
Secondary Th1 act	0.0	HUVEC IL-1beta	3.5
Secondary Th2 act	0.0	HUVEC IFN gamma	6.5
Secondary Tr1 act	3.3	HUVEC TNF alpha + IFN gamma	15.4
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	2.9
Secondary Th2 rest	5.2	HUVEC IL-11	9.0
Secondary Tr1 rest	0.0	Lung Microvascular EC none	2.7
Primary Th1 act	5.4	Lung Microvascular EC TNFalpha + IL-1beta	0.0
Primary Th2 act	0.0	Microvascular Dermal EC none	3.0
Primary Tr1 act	0.0	Microvascular Dermal EC TNFalpha + IL-1beta	10.7
Primary Th1 rest	3.3	Bronchial epithelium TNFalpha + IL1beta	18.0
Primary Th2 rest	5.1	Small airway epithelium none	0.0
Primary Tr1 rest	0.0	Small airway epithelium	79.0

		TNFalpha + IL-1beta	
CD45RA CD4 lymphocyte act	2.7	Coronary artery SMC rest	0.0
CD45RO CD4 lymphocyte act	0.0	Coronary artery SMC TNFalpha + IL-1beta	2.5
CD8 lymphocyte act	0.0	Astrocytes rest	11.3
Secondary CD8 lymphocyte rest	3.0	Astrocytes TNFalpha + IL-1beta	75.3
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	2.6
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	6.8
2ry Th1/Th2/Tr1_anti-CD95 CH11	1.6	CCD1106 (Keratinocytes) none	0.0
LAK cells rest	0.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	27.9
LAK cells IL-2	5.1	Liver cirrhosis	90.8
LAK cells IL-2+IL-12	3.0	Lupus kidney	51.8
LAK cells IL-2+IFN gamma	4.5	NCI-H292 none	28.1
LAK cells IL-2+ IL-18	23.2	NCI-H292 IL-4	10.6
LAK cells PMA/ionomycin	0.0	NCI-H292 IL-9	23.5
NK Cells IL-2 rest	6.2	NCI-H292 IL-13	4.8
Two Way MLR 3 day	12.1	NCI-H292 IFN gamma	10.3
Two Way MLR 5 day	3.1	HPAEC none	5.8
Two Way MLR 7 day	5.8	HPAEC TNF alpha + IL-1 beta	0.0
PBMC rest	0.0	Lung fibroblast none	3.7
PBMC PWM	0.0	Lung fibroblast TNF alpha + IL-1 beta	0.0
PBMC PHA-L	0.0	Lung fibroblast IL-4	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-9	6.4
Ramos (B cell) ionomycin	0.0	Lung fibroblast IL-13	3.2
B lymphocytes PWM	2.6	Lung fibroblast IFN gamma	10.5
B lymphocytes CD40L and IL-4	1.8	Dermal fibroblast CCD1070 rest	0.0
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 TNF alpha	13.7
EOL-1 dbcAMP PMA/ionomycin	0.0	Dermal fibroblast CCD1070 IL-1 beta	0.0
Dendritic cells none	6.5	Dermal fibroblast IFN gamma	0.0

Dendritic cells LPS	4.7	Dermal fibroblast IL-4	6.3
Dendritic cells anti-CD40	0.0	IBD Colitis 2	27.0
Monocytes rest	24.8	IBD Crohn's	9.3
Monocytes LPS	3.1	Colon	100.0
Macrophages rest	4.0	Lung	24.7
Macrophages LPS	0.0	Thymus	59.5
HUVEC none	6.5	Kidney	27.0
HUVEC starved	41.2		

CNS_neurodegeneration_v1.0 Summary: Ag3402 The CG59220-01 gene is expressed at low levels throughout the CNS, including in amygdala, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord. The GPCR family of receptors contains a large number of neurotransmitter receptors, including the dopamine, serotonin, α and β -adrenergic, acetylcholine muscarinic, histamine, peptide, and metabotropic glutamate receptors. GPCRs are excellent drug targets in various neurologic and psychiatric diseases. All antipsychotics have been shown to act at the dopamine D2 receptor; similarly novel antipsychotics also act at the serotonergic receptor, and often the muscarinic and adrenergic receptors as well. While the majority of antidepressants can be classified as selective serotonin reuptake inhibitors, blockade of the 5-HT1A and α 2 adrenergic receptors increases the effects of these drugs. The GPCRs are also of use as drug targets in the treatment of stroke. Blockade of the glutamate receptors may decrease the neuronal death resulting from excitotoxicity; further more the purinergic receptors have also been implicated as drug targets in the treatment of cerebral ischemia. The β -adrenergic receptors have been implicated in the treatment of ADHD with Ritalin, while the α -adrenergic receptors have been implicated in memory. Therefore this gene may be of use as a small molecule target for the treatment of any of the described diseases.

General_screening_panel_v1.4 Summary: Ag3402 The CG59220-01 gene represents a novel G-protein coupled receptor (GPCR) with highest expression in spinal cord sample (CT=31.12) and moderate expression in other samples from brain. Please see Panel CNS_neurodegeneration_v1.0 for discussion of utility of this gene in the central nervous system.

Low levels of expression of the CG59220-01 gene are also observed in areas outside of the central nervous system such as the, adipose tissue, fetal and adult heart, skeletal muscle, adrenal gland, pituitary gland, and thyroid suggesting the possibility of a wider role in

intercellular signaling. Therapeutic modulation of the expression or function of this gene may therefore be useful in the treatment of metabolic disorders, including obesity and diabetes.

Panel 4D Summary: Ag3402 The CG59220-01 gene represents a novel G-protein coupled receptor (GPCR) with highest expression in colon (CT=33.12). Thus expression of this gene can be used to distinguish these samples from other samples used in this panel. In addition, expression of this gene is low/undetectable (CT values > 35) in samples derived from IBD colitis and IBS Crohn's. Therefore, expression of this gene can be used to distinguish normal colon sample from the IBD colitis and IBD Crohn's sample used in this panel.

BN. CG59218-01: GPCR

Expression of gene CG59218-01 was assessed using the primer-probe set Ag3401, described in Table BNA. Results of the RTQ-PCR runs are shown in Tables BNB.

Table BNA. Probe Name Ag3401

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-gctggctactaggtttctcctt-3'	22	447	599
Probe	TET-5'-atcatcatgacctgtcatcctgaccag-3'- TAMRA	26	470	600
Reverse	5'-ttgatgtgggtatcacagaatg-3'	22	504	601

Table BNB. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3401, Run 165825154	Tissue Name	Rel. Exp.(%) Ag3401, Run 165825154
Secondary Th1 act	2.4	HUVEC IL-1beta	0.0
Secondary Th2 act	3.4	HUVEC IFN gamma	0.0
Secondary Tr1 act	8.4	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	3.1	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	0.0	HUVEC IL-11	0.0
Secondary Tr1 rest	0.0	Lung Microvascular EC none	0.0
Primary Th1 act	0.0	Lung Microvascular EC TNFalpha + IL-1beta	0.0
Primary Th2 act	3.1	Microvascular Dermal EC none	0.0
Primary Tr1 act	0.0	Microvascular Dermal EC	0.0

		TNFalpha + IL-1beta	
Primary Th1 rest	8.1	Bronchial epithelium TNFalpha + IL1beta	0.0
Primary Th2 rest	0.0	Small airway epithelium none	0.0
Primary Tr1 rest	3.3	Small airway epithelium TNFalpha + IL-1beta	0.0
CD45RA CD4 lymphocyte act	0.0	Coronary artery SMC rest	0.0
CD45RO CD4 lymphocyte act	0.0	Coronary artery SMC TNFalpha + IL-1beta	0.0
CD8 lymphocyte act	8.1	Astrocytes rest	5.7
Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFalpha + IL-1beta	0.0
Secondary CD8 lymphocyte act	1.0	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	0.0
2ry Th1/Th2/Tr1_anti- CD95 CH11	5.7	CCD1106 (Keratinocytes) none	0.0
LAK cells rest	0.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0
LAK cells IL-2	3.1	Liver cirrhosis	100.0
LAK cells IL-2+IL-12	3.2	Lupus kidney	0.0
LAK cells IL-2+IFN gamma	8.0	NCI-H292 none	0.0
LAK cells IL-2+ IL-18	4.3	NCI-H292 IL-4	0.0
LAK cells PMA/ionomycin	2.1	NCI-H292 IL-9	0.0
NK Cells IL-2 rest	0.0	NCI-H292 IL-13	0.0
Two Way MLR 3 day	0.0	NCI-H292 IFN gamma	0.0
Two Way MLR 5 day	0.0	HPAEC none	0.0
Two Way MLR 7 day	0.0	HPAEC TNF alpha + IL-1 beta	0.0
PBMC rest	0.0	Lung fibroblast none	0.0
PBMC PWM	3.3	Lung fibroblast TNF alpha + IL-1 beta	0.0
PBMC PHA-L	0.0	Lung fibroblast IL-4	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-9	0.0
Ramos (B cell) ionomycin	0.0	Lung fibroblast IL-13	0.0
B lymphocytes PWM	3.4	Lung fibroblast IFN gamma	0.0
B lymphocytes CD40L and IL-4	0.0	Dermal fibroblast CCD1070 rest	2.5

EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 TNF alpha	14.8
EOL-1 dbcAMP PMA/ionomycin	0.0	Dermal fibroblast CCD1070 IL-1 beta	0.0
Dendritic cells none	6.0	Dermal fibroblast IFN gamma	0.0
Dendritic cells LPS	0.0	Dermal fibroblast IL-4	0.0
Dendritic cells anti- CD40	0.0	IBD Colitis 2	17.1
Monocytes rest	0.0	IBD Crohn's	0.0
Monocytes LPS	6.1	Colon	0.0
Macrophages rest	0.0	Lung	0.0
Macrophages LPS	0.0	Thymus	0.0
HUVEC none	0.0	Kidney	3.2
HUVEC starved	0.0		

CNS_neurodegeneration_v1.0 Summary: Ag3401 Expression of the CG59218-01 gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.4 Summary: Ag3401 Expression of the CG59218-01 gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown). This gene product is most similar to members of the odorant receptor subfamily of GPCRs. Based on analogy to other odorant receptor genes, we predict that expression of this gene may be highest in nasal epithelium, a sample not represented on this panel.

Panel 4D Summary: Ag3401 Highest expression of the CG59218-01 gene is seen in the liver cirrhosis sample (CT=33.03). Thus, expression of this gene could be used to differentiate between this sample from the other samples on this panel and as a marker to detect the presence of liver cirrhosis. Furthermore, expression of this gene is not detected in normal liver in Panel 1.4, suggesting that its expression is unique to liver cirrhosis. This gene encodes a putative GPCR; therefore, antibodies or small molecule therapeutics could reduce or inhibit fibrosis that occurs in liver cirrhosis. In addition, antibodies to this putative GPCR could also be used for the diagnosis of liver cirrhosis.

BO. CG59211-01: GPCR

Expression of gene CG59211-01 was assessed using the primer-probe set Ag3397, described in Table BOA. Results of the RTQ-PCR runs are shown in Table BOB.

Table BOA. Probe Name Ag3397

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-tcacaggcatcctagacttgac-3'	22	645	602
Probe	TET-5'-tcatgtcctacatggtgatactgaaagca-3'- TAMRA	29	675	603
Reverse	5'-tttcttgatgctatgctcaaca-3'	22	705	604

Table BOB. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3397, Run 216822307	Tissue Name	Rel. Exp.(%) Ag3397, Run 216822307
Adipose	0.0	Renal ca. TK-10	0.0
Melanoma* Hs688(A).T	0.0	Bladder	0.0
Melanoma* Hs688(B).T	0.0	Gastric ca. (liver met.) NCI-N87	0.0
Melanoma* M14	0.0	Gastric ca. KATO III	0.0
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.0
Melanoma* SK- MEL-5	0.0	Colon ca. SW480	0.0
Squamous cell carcinoma SCC-4	0.0	Colon ca.* (SW480 met) SW620	0.7
Testis Pool	0.0	Colon ca. HT29	0.0
Prostate ca.* (bone met) PC-3	0.0	Colon ca. HCT-116	0.0
Prostate Pool	0.0	Colon ca. CaCo-2	0.0
Placenta	0.0	Colon cancer tissue	0.0
Uterus Pool	0.0	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	0.0	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV- 3	0.0	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	0.0	Colon Pool	0.6
Ovarian ca. OVCAR-5	0.0	Small Intestine Pool	0.0
Ovarian ca. IGROV- 1	0.0	Stomach Pool	0.0
Ovarian ca. OVCAR-8	0.0	Bone Marrow Pool	0.0
Ovary	0.0	Fetal Heart	0.5
Breast ca. MCF-7	0.0	Heart Pool	0.5
Breast ca. MDA- MB-231	0.0	Lymph Node Pool	0.0

Breast ca. BT 549	0.0	Fetal Skeletal Muscle	0.0
Breast ca. T47D	0.0	Skeletal Muscle Pool	0.0
Breast ca. MDA-N	0.0	Spleen Pool	0.0
Breast Pool	0.6	Thymus Pool	0.0
Trachea	0.0	CNS cancer (glio/astro) U87-MG	0.0
Lung	0.0	CNS cancer (glio/astro) U-118-MG	0.0
Fetal Lung	0.0	CNS cancer (neuro;met) SK-N-AS	0.8
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF- 539	0.0
Lung ca. LX-1	0.0	CNS cancer (astro) SNB-75	0.0
Lung ca. NCI-H146	2.6	CNS cancer (glio) SNB-19	0.0
Lung ca. SHP-77	100.0	CNS cancer (glio) SF- 295	0.0
Lung ca. A549	0.0	Brain (Amygdala) Pool	0.0
Lung ca. NCI-H526	0.0	Brain (cerebellum)	0.0
Lung ca. NCI-H23	0.0	Brain (fetal)	0.0
Lung ca. NCI-H460	0.0	Brain (Hippocampus) Pool	0.0
Lung ca. HOP-62	0.0	Cerebral Cortex Pool	0.0
Lung ca. NCI-H522	0.0	Brain (Substantia nigra) Pool	0.0
Liver	0.0	Brain (Thalamus) Pool	0.0
Fetal Liver	0.0	Brain (whole)	0.9
Liver ca. HepG2	0.0	Spinal Cord Pool	0.0
Kidney Pool	0.9	Adrenal Gland	0.0
Fetal Kidney	3.3	Pituitary gland Pool	0.0
Renal ca. 786-0	0.0	Salivary Gland	0.0
Renal ca. A498	0.0	Thyroid (female)	0.0
Renal ca. ACHN	0.0	Pancreatic ca. CAPAN2	0.0
Renal ca. UO-31	0.0	Pancreas Pool	0.0

CNS_neurodegeneration_v1.0 Summary: Ag3397 Expression of the CG59211-01 gene is low/undetectable (CT values > 35) across the samples in this panel. (Data not shown.) This gene encodes a G protein-coupled receptor (GPCR), a type of cell surface receptor involved in signal transduction. It is most similar to members of the odorant receptor subfamily of GPCRs. Based on analogy to other odorant receptor genes, we predict that expression of this gene may be highest in nasal epithelium, a sample not represented on this panel.

General_screening_panel_v1.4 Summary: Ag3397 Significant expression of the CG59211-01 gene is seen exclusively in one of the lung cancer sample (CT = 32.29). Therefore, expression of this gene may be used to distinguish this sample from other samples on this panel and as a marker for lung cancer. There is an increasing awareness that some GPCRs can regulate proliferative signaling pathways and that chronic stimulation or mutational activation of receptors can lead to oncogenic transformation. Activating mutations in GPCRs are associated with several types of human tumors and some receptors exhibit potent oncogenic activity due to agonist overexpression (Whitehead et al., 2001). Therefore, therapeutic modulation of the activity of the GPCR encoded by this gene may be beneficial in the treatment of lung cancer.

References:

1. Whitehead IP, Zohn IE, Der CJ. (2001) Rho GTPase-dependent transformation by G protein-coupled receptors. *Oncogene* 2001 Mar 26;20(13):1547-55

Panel 4D Summary: Ag3397 Expression of the CG59211-01 gene is low/undetectable (CT values > 35) across the samples in this panel. (Data not shown.)

BP. CG59276-01: Dihydroorotate dehydrogenase

Expression of gene CG59276-01 was assessed using the primer-probe set Ag3524, described in Table BPA. Results of the RTQ-PCR runs are shown in Tables BPB, BPC, BPD, BPE and BPF.

Table BPA. Probe Name Ag3524

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-ttcaggcactgttctttgactt-3'	22	1439	605
Probe	5'-aacagatctttgcaacactttccaagg-3'- TAMRA	26	1472	606
Reverse	5'-tgagggagtggtaacactgtgt-3'	22	1498	607

Table BPB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3524, Run 206915926	Tissue Name	Rel. Exp.(%) Ag3524, Run 206915926
AD 1 Hippo	26.8	Control (Path) 3	18.9

		Temporal Ctx	
AD 2 Hippo	30.8	Control (Path) 4 Temporal Ctx	51.4
AD 3 Hippo	25.3	AD 1 Occipital Ctx	37.1
AD 4 Hippo	38.2	AD 2 Occipital Ctx (Missing)	0.0
AD 5 Hippo	77.4	AD 3 Occipital Ctx	16.5
AD 6 Hippo	83.5	AD 4 Occipital Ctx	40.9
Control 2 Hippo	43.8	AD 5 Occipital Ctx	33.9
Control 4 Hippo	20.6	AD 6 Occipital Ctx	17.0
Control (Path) 3 Hippo	17.6	Control 1 Occipital Ctx	6.3
AD 1 Temporal Ctx	37.1	Control 2 Occipital Ctx	74.7
AD 2 Temporal Ctx	31.2	Control 3 Occipital Ctx	22.1
AD 3 Temporal Ctx	6.5	Control 4 Occipital Ctx	25.7
AD 4 Temporal Ctx	79.6	Control (Path) 1 Occipital Ctx	89.5
AD 5 Inf Temporal Ctx	97.9	Control (Path) 2 Occipital Ctx	18.4
AD 5 Sup Temporal Ctx	56.3	Control (Path) 3 Occipital Ctx	11.2
AD 6 Inf Temporal Ctx	100.0	Control (Path) 4 Occipital Ctx	24.8
AD 6 Sup Temporal Ctx	66.9	Control 1 Parietal Ctx	26.8
Control 1 Temporal Ctx	10.6	Control 2 Parietal Ctx	68.3
Control 2 Temporal Ctx	13.4	Control 3 Parietal Ctx	28.1
Control 3 Temporal Ctx	25.9	Control (Path) 1 Parietal Ctx	58.6
Control 3 Temporal Ctx	36.6	Control (Path) 2 Parietal Ctx	51.4
Control (Path) 1 Temporal Ctx	80.7	Control (Path) 3 Parietal Ctx	6.9
Control (Path) 2 Temporal Ctx	76.8	Control (Path) 4 Parietal Ctx	54.7

Table BPC. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3524, Run 213390931	Tissue Name	Rel. Exp.(%) Ag3524, Run 213390931
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Adipose	6.2	Renal ca. TK-10	9.3
Melanoma* Hs688(A).T	3.1	Bladder	22.1
Melanoma* Hs688(B).T	9.2	Gastric ca. (liver met.) NCI-N87	24.8
Melanoma* M14	0.9	Gastric ca. KATO III	0.0
Melanoma* LOXIMVI	0.4	Colon ca. SW-948	1.2
Melanoma* SK- MEL-5	0.7	Colon ca. SW480	4.2
Squamous cell carcinoma SCC-4	0.0	Colon ca.* (SW480 met) SW620	10.5
Testis Pool	11.3	Colon ca. HT29	1.1
Prostate ca.* (bone met) PC-3	3.1	Colon ca. HCT-116	5.3
Prostate Pool	8.7	Colon ca. CaCo-2	8.5
Placenta	1.3	Colon cancer tissue	7.2
Uterus Pool	2.9	Colon ca. SW1116	1.4
Ovarian ca. OVCAR-3	6.9	Colon ca. Colo-205	1.6
Ovarian ca. SK-OV- 3	11.7	Colon ca. SW-48	1.7
Ovarian ca. OVCAR-4	0.2	Colon Pool	12.6
Ovarian ca. OVCAR-5	8.5	Small Intestine Pool	20.9
Ovarian ca. IGROV- 1	2.5	Stomach Pool	13.2
Ovarian ca. OVCAR-8	4.1	Bone Marrow Pool	8.7
Ovary	15.3	Fetal Heart	9.5
Breast ca. MCF-7	3.4	Heart Pool	11.3
Breast ca. MDA- MB-231	3.1	Lymph Node Pool	27.2
Breast ca. BT 549	23.5	Fetal Skeletal Muscle	9.1
Breast ca. T47D	19.5	Skeletal Muscle Pool	6.7
Breast ca. MDA-N	0.3	Spleen Pool	8.9
Breast Pool	25.2	Thymus Pool	18.2
Trachea	12.6	CNS cancer (glio/astro) U87-MG	8.7
Lung	13.3	CNS cancer (glio/astro) U-118-MG	7.5
Fetal Lung	41.8	CNS cancer (neuro;met) SK-N-AS	21.3

Lung ca. NCI-N417	0.0	CNS cancer (astro) SF-539	2.4
Lung ca. LX-1	32.1	CNS cancer (astro) SNB-75	97.9
Lung ca. NCI-H146	1.4	CNS cancer (glio) SNB-19	3.0
Lung ca. SHP-77	2.3	CNS cancer (glio) SF-295	26.1
Lung ca. A549	5.4	Brain (Amygdala) Pool	4.1
Lung ca. NCI-H526	0.4	Brain (cerebellum)	33.0
Lung ca. NCI-H23	100.0	Brain (fetal)	25.5
Lung ca. NCI-H460	7.9	Brain (Hippocampus) Pool	7.5
Lung ca. HOP-62	4.2	Cerebral Cortex Pool	7.7
Lung ca. NCI-H522	1.4	Brain (Substantia nigra) Pool	5.8
Liver	1.4	Brain (Thalamus) Pool	11.7
Fetal Liver	9.3	Brain (whole)	9.5
Liver ca. HepG2	5.2	Spinal Cord Pool	10.5
Kidney Pool	40.3	Adrenal Gland	9.1
Fetal Kidney	40.1	Pituitary gland Pool	2.0
Renal ca. 786-0	12.9	Salivary Gland	8.3
Renal ca. A498	3.4	Thyroid (female)	2.5
Renal ca. ACHN	5.4	Pancreatic ca. CAPAN2	9.3
Renal ca. UO-31	7.2	Pancreas Pool	20.9

Table BPD. Panel 2D

Tissue Name	Rel. Exp.(%) Ag3524, Run 169590472	Tissue Name	Rel. Exp.(%) Ag3524, Run 169590472
Normal Colon	28.1	Kidney Margin 8120608	1.8
CC Well to Mod Diff (ODO3866)	2.4	Kidney Cancer 8120613	2.7
CC Margin (ODO3866)	1.4	Kidney Margin 8120614	8.0
CC Gr.2 rectosigmoid (ODO3868)	3.5	Kidney Cancer 9010320	6.0
CC Margin (ODO3868)	1.1	Kidney Margin 9010321	11.7
CC Mod Diff (ODO3920)	9.9	Normal Uterus	4.8
CC Margin (ODO3920)	6.0	Uterus Cancer 064011	2.3
CC Gr.2 ascend colon	12.3	Normal Thyroid	6.6

(ODO3921)			
CC Margin (ODO3921)	3.1	Thyroid Cancer 064010	0.5
CC from Partial Hepatectomy (ODO4309) Mets	12.8	Thyroid Cancer A302152	2.1
Liver Margin (ODO4309)	34.6	Thyroid Margin A302153	9.2
Colon mets to lung (OD04451-01)	12.2	Normal Breast	13.6
Lung Margin (OD04451- 02)	2.9	Breast Cancer (OD04566)	6.4
Normal Prostate 6546-1	9.9	Breast Cancer (OD04590-01)	9.8
Prostate Cancer (OD04410)	16.6	Breast Cancer Mets (OD04590-03)	14.0
Prostate Margin (OD04410)	15.4	Breast Cancer Metastasis (OD04655-05)	5.3
Prostate Cancer (OD04720-01)	20.6	Breast Cancer 064006	11.2
Prostate Margin (OD04720-02)	16.6	Breast Cancer 1024	31.6
Normal Lung 061010	27.2	Breast Cancer 9100266	8.0
Lung Met to Muscle (ODO4286)	3.5	Breast Margin 9100265	4.6
Muscle Margin (ODO4286)	6.7	Breast Cancer A209073	4.1
Lung Malignant Cancer (OD03126)	3.7	Breast Margin A209073	8.4
Lung Margin (OD03126)	10.8	Normal Liver	100.0
Lung Cancer (OD04404)	4.1	Liver Cancer 064003	44.4
Lung Margin (OD04404)	4.3	Liver Cancer 1025	47.0
Lung Cancer (OD04565)	0.9	Liver Cancer 1026	0.9
Lung Margin (OD04565)	8.5	Liver Cancer 6004-T	59.5
Lung Cancer (OD04237- 01)	13.2	Liver Tissue 6004-N	6.6
Lung Margin (OD04237- 02)	4.5	Liver Cancer 6005-T	1.5
Ocular Mel Met to Liver (ODO4310)	6.7	Liver Tissue 6005-N	0.5
Liver Margin (ODO4310)	6.7	Normal Bladder	21.5
Melanoma Mets to Lung (OD04321)	3.9	Bladder Cancer 1023	0.9

Lung Margin (OD04321)	4.7	Bladder Cancer A302173	5.9
Normal Kidney	35.8	Bladder Cancer (OD04718-01)	5.5
Kidney Ca, Nuclear grade 2 (OD04338)	18.0	Bladder Normal Adjacent (OD04718- 03)	6.5
Kidney Margin (OD04338)	14.1	Normal Ovary	4.5
Kidney Ca Nuclear grade 1/2 (OD04339)	13.7	Ovarian Cancer 064008	3.7
Kidney Margin (OD04339)	9.9	Ovarian Cancer (OD04768-07)	11.0
Kidney Ca, Clear cell type (OD04340)	10.8	Ovary Margin (OD04768-08)	1.1
Kidney Margin (OD04340)	12.7	Normal Stomach	7.6
Kidney Ca, Nuclear grade 3 (OD04348)	0.5	Gastric Cancer 9060358	3.3
Kidney Margin (OD04348)	10.6	Stomach Margin 9060359	4.0
Kidney Cancer (OD04622-01)	0.9	Gastric Cancer 9060395	8.2
Kidney Margin (OD04622-03)	1.6	Stomach Margin 9060394	5.5
Kidney Cancer (OD04450-01)	4.2	Gastric Cancer 9060397	3.8
Kidney Margin (OD04450-03)	5.4	Stomach Margin 9060396	0.9
Kidney Cancer 8120607	1.0	Gastric Cancer 064005	14.5

Table BPE. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3524, Run 166445583	Tissue Name	Rel. Exp.(%) Ag3524, Run 166445583
Secondary Th1 act	13.9	HUVEC IL-1beta	2.4
Secondary Th2 act	17.1	HUVEC IFN gamma	16.4
Secondary Tr1 act	15.4	HUVEC TNF alpha + IFN gamma	4.8
Secondary Th1 rest	36.6	HUVEC TNF alpha + IL4	3.8
Secondary Th2 rest	19.1	HUVEC IL-11	6.1
Secondary Tr1 rest	28.7	Lung Microvascular EC none	9.2

Primary Th1 act	10.2	Lung Microvascular EC TNFalpha + IL-1beta	5.0
Primary Th2 act	18.2	Microvascular Dermal EC none	14.5
Primary Tr1 act	28.5	Microvascular Dermal EC TNFalpha + IL-1beta	10.4
Primary Th1 rest	100.0	Bronchial epithelium TNFalpha + IL1beta	6.1
Primary Th2 rest	42.3	Small airway epithelium none	3.3
Primary Tr1 rest	35.8	Small airway epithelium TNFalpha + IL-1beta	29.3
CD45RA CD4 lymphocyte act	14.6	Coronary artery SMC rest	5.6
CD45RO CD4 lymphocyte act	28.7	Coronary artery SMC TNFalpha + IL-1beta	3.4
CD8 lymphocyte act	17.7	Astrocytes rest	12.1
Secondary CD8 lymphocyte rest	23.7	Astrocytes TNFalpha + IL-1beta	11.5
Secondary CD8 lymphocyte act	12.7	KU-812 (Basophil) rest	23.2
CD4 lymphocyte none	22.2	KU-812 (Basophil) PMA/ionomycin	37.1
2ry Th1/Th2/Tr1 _anti- CD95 CH11	39.5	CCD1106 (Keratinocytes) none	5.0
LAK cells rest	17.9	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	41.5
LAK cells IL-2	41.2	Liver cirrhosis	37.9
LAK cells IL-2+IL-12	31.0	Lupus kidney	21.8
LAK cells IL-2+IFN gamma	47.0	NCI-H292 none	25.0
LAK cells IL-2+ IL-18	44.8	NCI-H292 IL-4	21.3
LAK cells PMA/ionomycin	5.3	NCI-H292 IL-9	21.6
NK Cells IL-2 rest	17.8	NCI-H292 IL-13	9.2
Two Way MLR 3 day	47.6	NCI-H292 IFN gamma	10.6
Two Way MLR 5 day	13.0	HPAEC none	16.5
Two Way MLR 7 day	18.8	HPAEC TNF alpha + IL-1 beta	4.0
PBMC rest	7.6	Lung fibroblast none	30.4
PBMC PWM	24.7	Lung fibroblast TNF alpha + IL-1 beta	24.3
PBMC PHA-L	4.9	Lung fibroblast IL-4	23.8
Ramos (B cell) none	19.5	Lung fibroblast IL-9	14.6
Ramos (B cell)	10.7	Lung fibroblast IL-13	17.1

ionomycin			
B lymphocytes PWM	22.8	Lung fibroblast IFN gamma	24.1
B lymphocytes CD40L and IL-4	40.1	Dermal fibroblast CCD1070 rest	20.3
EOL-1 dbcAMP	15.9	Dermal fibroblast CCD1070 TNF alpha	22.4
EOL-1 dbcAMP PMA/ionomycin	11.7	Dermal fibroblast CCD1070 IL-1 beta	0.6
Dendritic cells none	22.2	Dermal fibroblast IFN gamma	10.6
Dendritic cells LPS	14.5	Dermal fibroblast IL-4	11.8
Dendritic cells anti-CD40	23.5	IBD Colitis 2	7.3
Monocytes rest	37.9	IBD Crohn's	8.0
Monocytes LPS	15.8	Colon	54.0
Macrophages rest	10.2	Lung	9.7
Macrophages LPS	5.0	Thymus	39.5
HUVEC none	17.3	Kidney	63.7
HUVEC starved	11.8		

Table BPF. Panel 5 Islet

Tissue Name	Rel. Exp.(%) Ag3524, Run 242386392	Tissue Name	Rel. Exp.(%) Ag3524, Run 242386392
97457_Patient-02go_adipose	66.0	94709_Donor 2 AM - A_adipose	9.0
97476_Patient-07sk_skeletal muscle	10.7	94710_Donor 2 AM - B_adipose	9.8
97477_Patient-07ut_uterus	9.4	94711_Donor 2 AM - C_adipose	8.1
97478_Patient-07pl_placenta	7.8	94712_Donor 2 AD - A_adipose	17.8
99167_Bayer Patient 1	10.2	94713_Donor 2 AD - B_adipose	27.0
97482_Patient-08ut_uterus	0.0	94714_Donor 2 AD - C_adipose	43.5
97483_Patient-08pl_placenta	0.0	94742_Donor 3 U - A_Mesenchymal Stem Cells	0.0
97486_Patient-09sk_skeletal muscle	0.0	94743_Donor 3 U - B_Mesenchymal Stem Cells	0.0
97487_Patient-09ut_uterus	0.0	94730_Donor 3 AM - A_adipose	16.8
97488_Patient-09pl_placenta	17.0	94731_Donor 3 AM - B_adipose	7.8

97492_Patient-10ut_uterus	28.1	94732_Donor 3 AM - C_adipose	18.0
97493_Patient-10pl_placenta	25.3	94733_Donor 3 AD - A_adipose	0.0
97495_Patient-11go_adipose	61.6	94734_Donor 3 AD - B_adipose	0.0
97496_Patient-11sk_skeletal muscle	28.5	94735_Donor 3 AD - C_adipose	18.9
97497_Patient-11ut_uterus	16.2	77138_Liver_HepG2untreated	15.8
97498_Patient-11pl_placenta	5.0	73556_Heart_Cardiac stromal cells (primary)	9.7
97500_Patient-12go_adipose	100.0	81735_Small Intestine	62.9
97501_Patient-12sk_skeletal muscle	42.6	72409_Kidney_Proximal Convoluted Tubule	24.0
97502_Patient-12ut_uterus	41.8	82685_Small intestine_Duodenum	32.8
97503_Patient-12pl_placenta	0.0	90650_Adrenal_Adrenocortical adenoma	0.0
94721_Donor 2 U - A_Mesenchymal Stem Cells	0.0	72410_Kidney_HRCE	39.8
94722_Donor 2 U - B_Mesenchymal Stem Cells	0.0	72411_Kidney_HRE	21.8
94723_Donor 2 U - C_Mesenchymal Stem Cells	0.0	73139_Uterus_Uterine smooth muscle cells	8.1

CNS_neurodegeneration_v1.0 Summary: Ag3524 No differential expression of the CG59276-01 gene is detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. However, as observed in panel 1.4 this gene is expressed at low levels throughout the CNS, including in amygdala, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord. Therefore, this gene may play a role in central nervous system disorders such as Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

General_screening_panel_v1.4 Summary: Ag3524 Expression of the CG59276-01 gene is highest in a sample derived from a brain and lung cancer cell lines (CTs = 29). Thus, the expression of this gene could be used to distinguish these samples from the other samples in the panel. The CG59276-01 gene encodes a dihydroorotate dehydrogenase (DHODH)

homolog. DHODH is an enzyme involved in the pathway for pyrimidine production. Drugs known to inhibit DHODH activity, such as brequinar sodium (Dup-785), have been shown to have anti-tumor activities (ref. 1). Therefore, therapeutic modulation of the activity of this gene encoded by this gene may be beneficial in the treatment of CNS and lung cancer. In addition, low to moderate expression of this gene is seen in all of the samples on this panel. Therefore, this gene may be playing an important role in cellular function.

This gene is expressed at low to moderate levels in a number of tissues with metabolic or endocrine function, including adipose, adrenal gland, gastrointestinal tract, pancreas, and skeletal muscle. Therefore, therapeutic modulation of the activity of this gene may prove useful in the treatment of endocrine/metabolically related diseases, such as obesity and diabetes.

Recently, it has been demonstrated that down regulation of DHODH mRNA using RNA interference (RNAi) may inhibit growth of *Plasmodium falciparum* (ref 2).

References:

1. Braakhuis BJ, van Dongen GA, Peters GJ, van Walsum M, Snow GB (1990) Antitumor activity of brequinar sodium (Dup-785) against human head and neck squamous cell carcinoma xenografts. *Cancer Lett* 49(2):133-7.
2. McRobert L, McConkey GA.(2002) RNA interference (RNAi) inhibits growth of *Plasmodium falciparum*. *Mol Biochem Parasitol* 119(2):273-8

Panel 2D Summary: Ag3524 The expression of this gene appears to be highest in a sample derived from a normal liver tissue (CT=30.3). In addition, there appears to be substantial expression in other samples derived from liver cancers and breast cancers. Thus, the expression of this gene could be used to distinguish normal liver tissue from other samples in the panel. Moreover, therapeutic modulation of this gene, through the use of small molecule drugs, protein therapeutics or antibodies could be of benefit in the treatment of liver or breast cancer.

Panel 4D Summary: Ag3524 Highest expression of the CG59276-01 gene is detected in resting primary Th1 cells (CT=30.03). In addition, the expression of this gene is significantly reduced in activated primary Th1 cells, suggesting a regulatory role for this gene in T-cell

activation. The CG59276-01 encodes a dihydroorotate dehydrogenase, an enzyme involved in the pathway for pyrimidine production. Recently, an inhibitor of this enzyme, leflunomide has been shown to be an effective treatment for rheumatoid arthritis (ref 1). Therefore, therapeutics designed with the protein encoded for by this transcript could be important in regulating T cell function and treating T cell mediated diseases such as asthma, rheumatoid arthritis, psoriasis, IBD, and systemic lupus erythematosus.

Overall, this gene is expressed at low to moderate levels in a wide range of cell types of significance in the immune response in health and disease. These cells include members of the T-cell, B-cell, endothelial cell, macrophage/monocyte, and peripheral blood mononuclear cell family, as well as epithelial and fibroblast cell types from lung and skin, and normal tissues represented by colon, lung, thymus and kidney. This ubiquitous pattern of expression suggests that this gene product may be involved in homeostatic processes for these and other cell types and tissues. This pattern is in agreement with the expression profile in General_screening_panel_v1.4 and also suggests a role for the gene product in cell survival and proliferation.

Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

Reference:

1. Schattenkirchner M. (2000) The use of leflunomide in the treatment of rheumatoid arthritis: an experimental and clinical review. *Immunopharmacology* 47(2-3):291-8

Panel 5 Islet Summary: Ag3524 This gene has a low level of expression in adipose tissue (CTs=33-35). Thus, this gene product may be a small molecule drug for the treatment of obesity and obesity-related diseases, including Type 2 diabetes.

BQ. CG59268-01: KIAA2372

Expression of gene CG59268-01 was assessed using the primer-probe set Ag3523, described in Table BQA. Results of the RTQ-PCR runs are shown in Tables BQB and BQC.

Table BQA. Probe Name Ag3523

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-tactcttttggcttgatggaaa-3'	22	556	608
Probe	TET-5'-ccaacttctacgaccaggcagaaaa-3'- TAMRA	25	578	609
Reverse	5'-gacaaagagttggtgcctcttt-3'	22	610	610

Table BQB. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3523, Run 216874716	Tissue Name	Rel. Exp.(%) Ag3523, Run 216874716
Adipose	47.6	Renal ca. TK-10	62.9
Melanoma* Hs688(A).T	4.0	Bladder	25.2
Melanoma* Hs688(B).T	0.0	Gastric ca. (liver met.) NCI-N87	40.1
Melanoma* M14	15.4	Gastric ca. KATO III	0.0
Melanoma* LOXIMVI	0.8	Colon ca. SW-948	0.0
Melanoma* SK- MEL-5	39.5	Colon ca. SW480	9.7
Squamous cell carcinoma SCC-4	0.0	Colon ca.* (SW480 met) SW620	10.2
Testis Pool	35.8	Colon ca. HT29	27.2
Prostate ca.* (bone met) PC-3	8.5	Colon ca. HCT-116	52.5
Prostate Pool	0.0	Colon ca. CaCo-2	31.2
Placenta	0.0	Colon cancer tissue	14.1
Uterus Pool	0.0	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	0.0	Colon ca. Colo-205	12.2
Ovarian ca. SK-OV- 3	16.3	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	10.3	Colon Pool	0.0
Ovarian ca. OVCAR-5	47.6	Small Intestine Pool	3.9
Ovarian ca. IGROV- 1	0.0	Stomach Pool	4.3
Ovarian ca. OVCAR-8	1.5	Bone Marrow Pool	0.0
Ovary	0.0	Fetal Heart	4.2

Breast ca. MCF-7	6.0	Heart Pool	4.2
Breast ca. MDA-MB-231	8.8	Lymph Node Pool	0.0
Breast ca. BT 549	33.4	Fetal Skeletal Muscle	0.0
Breast ca. T47D	62.9	Skeletal Muscle Pool	5.1
Breast ca. MDA-N	8.8	Spleen Pool	0.0
Breast Pool	0.0	Thymus Pool	0.0
Trachea	0.0	CNS cancer (glio/astro) U87-MG	9.0
Lung	0.0	CNS cancer (glio/astro) U-118-MG	33.2
Fetal Lung	15.1	CNS cancer (neuro;met) SK-N-AS	23.5
Lung ca. NCI-N417	3.5	CNS cancer (astro) SF-539	11.0
Lung ca. LX-1	3.7	CNS cancer (astro) SNB-75	13.8
Lung ca. NCI-H146	0.0	CNS cancer (glio) SNB-19	20.7
Lung ca. SHP-77	11.0	CNS cancer (glio) SF-295	30.1
Lung ca. A549	6.3	Brain (Amygdala) Pool	0.0
Lung ca. NCI-H526	0.0	Brain (cerebellum)	0.0
Lung ca. NCI-H23	3.8	Brain (fetal)	4.5
Lung ca. NCI-H460	13.5	Brain (Hippocampus) Pool	4.6
Lung ca. HOP-62	4.0	Cerebral Cortex Pool	0.0
Lung ca. NCI-H522	9.2	Brain (Substantia nigra) Pool	4.4
Liver	4.5	Brain (Thalamus) Pool	0.0
Fetal Liver	0.0	Brain (whole)	0.0
Liver ca. HepG2	100.0	Spinal Cord Pool	0.0
Kidney Pool	6.5	Adrenal Gland	8.3
Fetal Kidney	17.9	Pituitary gland Pool	6.6
Renal ca. 786-0	38.7	Salivary Gland	16.3
Renal ca. A498	3.2	Thyroid (female)	0.0
Renal ca. ACHN	9.0	Pancreatic ca. CAPAN2	16.5
Renal ca. UO-31	0.0	Pancreas Pool	11.3

Table BQC. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3523, Run 166407138	Tissue Name	Rel. Exp.(%) Ag3523, Run 166407138
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Secondary Th1 act	11.3	HUVEC IL-1beta	1.5
Secondary Th2 act	2.7	HUVEC IFN gamma	0.0
Secondary Tr1 act	9.5	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	1.3	HUVEC IL-11	5.1
Secondary Tr1 rest	1.7	Lung Microvascular EC none	0.0
Primary Th1 act	13.1	Lung Microvascular EC TNFalpha + IL-1beta	0.0
Primary Th2 act	10.8	Microvascular Dermal EC none	1.0
Primary Tr1 act	7.5	Microvascular Dermal EC TNFalpha + IL-1beta	1.6
Primary Th1 rest	1.4	Bronchial epithelium TNFalpha + IL1beta	0.0
Primary Th2 rest	0.0	Small airway epithelium none	1.0
Primary Tr1 rest	2.6	Small airway epithelium TNFalpha + IL-1beta	4.4
CD45RA CD4 lymphocyte act	0.0	Coronary artery SMC rest	0.0
CD45RO CD4 lymphocyte act	8.0	Coronary artery SMC TNFalpha + IL-1beta	0.0
CD8 lymphocyte act	0.0	Astrocytes rest	0.0
Secondary CD8 lymphocyte rest	1.5	Astrocytes TNFalpha + IL-1beta	0.0
Secondary CD8 lymphocyte act	3.1	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	1.0	KU-812 (Basophil) PMA/ionomycin	8.1
2ry Th1/Th2/Tr1_anti-CD95 CH11	3.7	CCD1106 (Keratinocytes) none	4.0
LAK cells rest	7.2	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	2.2
LAK cells IL-2	0.0	Liver cirrhosis	15.3
LAK cells IL-2+IL-12	8.9	Lupus kidney	5.0
LAK cells IL-2+IFN gamma	12.2	NCI-H292 none	1.0
LAK cells IL-2+ IL-18	4.7	NCI-H292 IL-4	0.6
LAK cells PMA/ionomycin	1.4	NCI-H292 IL-9	1.6
NK Cells IL-2 rest	7.9	NCI-H292 IL-13	1.5
Two Way MLR 3 day	0.0	NCI-H292 IFN gamma	1.2
Two Way MLR 5 day	0.0	HPAEC none	0.0

Two Way MLR 7 day	0.0	HPAEC TNF alpha + IL-1 beta	0.0
PBMC rest	5.5	Lung fibroblast none	0.0
PBMC PWM	2.6	Lung fibroblast TNF alpha + IL-1 beta	0.0
PBMC PHA-L	0.0	Lung fibroblast IL-4	3.9
Ramos (B cell) none	0.0	Lung fibroblast IL-9	0.0
Ramos (B cell) ionomycin	0.0	Lung fibroblast IL-13	0.0
B lymphocytes PWM	8.2	Lung fibroblast IFN gamma	0.0
B lymphocytes CD40L and IL-4	1.5	Dermal fibroblast CCD1070 rest	0.0
EOL-1 dbcAMP	4.5	Dermal fibroblast CCD1070 TNF alpha	13.9
EOL-1 dbcAMP PMA/ionomycin	10.8	Dermal fibroblast CCD1070 IL-1 beta	0.4
Dendritic cells none	0.0	Dermal fibroblast IFN gamma	0.0
Dendritic cells LPS	0.0	Dermal fibroblast IL-4	0.0
Dendritic cells anti-CD40	0.0	IBD Colitis 2	0.0
Monocytes rest	11.5	IBD Crohn's	66.0
Monocytes LPS	6.4	Colon	100.0
Macrophages rest	4.5	Lung	0.0
Macrophages LPS	1.4	Thymus	38.4
HUVEC none	1.9	Kidney	0.0
HUVEC starved	1.6		

CNS_neurodegeneration_v1.0 Summary: Ag3523 Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.4 Summary: Ag3523 Expression of the CG59268-01 gene is highest in sample derived from liver cancer cell line (CT=32.55). Therefore, expression of this gene may be used to distinguish liver cancers from the other samples on this panel. In addition, low levels of expression of this gene are also observed in one of the ovarian cancer, 2 of the breast cancer, 2 of the renal cancer, bladder, gastric cancer, 3 of the colon cancer, and 4 of the CNS cancer samples. Therefore, therapeutic modulation of the activity of this gene product may be beneficial in the treatment of these cancers.

Among the tissues with metabolic or endocrine function, this gene is expressed at low levels in adipose tissue sample. Adipose tissue has several crucial roles including (i) mobilization from stores of fatty acids as an energy source, (ii) catabolism of lipoproteins such as very-low-density lipoprotein and (iii) synthesis and release of hormonal signals such as leptin and interleukin-6 (Coppack et al., 2001). Therefore, therapeutic modulation of the activity of this gene may prove useful in the treatment of endocrine/metabolically related diseases, such as obesity, hyperlipidemia, and insulin resistance.

References:

1. Coppack SW, Patel JN, Lawrence VJ. (2001) Nutritional regulation of lipid metabolism in human adipose tissue. *Exp Clin Endocrinol Diabetes* ;109(Suppl 2):S202-S214

Panel 4D Summary: Ag3523 Expression of the CG59268-01 gene is highest in sample derived from colon (CT=31.56). Therefore, expression of this gene may be used to distinguish colon sample from the other samples on this panel. In addition, significant expression of this gene is also observed in IBD Crohn's sample (CT=32.16). Thus, expression of this gene in colon and Crohn's sample can be used to distinguish these two samples from IBD Colitis 2 sample. In addition, therapeutic modulation of the activity of this gene product may be beneficial in the treatment of IBD Crohn's disease.

BR. CG59549-01: H326 like

Expression of gene CG59549-01 was assessed using the primer-probe set Ag3464, described in Table BRA. Results of the RTQ-PCR runs are shown in Tables BRB and BRC.

Table BRA. Probe Name Ag3464

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-gtgcgtcacctgttacagaga-3'	21	1678	611
Probe	TET-5'-ctcatcaaccggtggagagatcat-3'- TAMRA	26	1700	612
Reverse	5'-ctcttcttctcatctgggaactca-3'	22	1731	613

Table BRB. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3464, Run 217067408	Tissue Name	Rel. Exp.(%) Ag3464, Run 217067408
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Adipose	0.0	Renal ca. TK-10	0.0
Melanoma* Hs688(A).T	0.0	Bladder	0.0
Melanoma* Hs688(B).T	0.0	Gastric ca. (liver met.) NCI-N87	1.6
Melanoma* M14	1.0	Gastric ca. KATO III	2.1
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.0
Melanoma* SK- MEL-5	23.8	Colon ca. SW480	2.6
Squamous cell carcinoma SCC-4	0.0	Colon ca.* (SW480 met) SW620	0.0
Testis Pool	22.8	Colon ca. HT29	0.0
Prostate ca.* (bone met) PC-3	0.0	Colon ca. HCT-116	0.0
Prostate Pool	0.0	Colon ca. CaCo-2	0.0
Placenta	0.0	Colon cancer tissue	0.3
Uterus Pool	0.0	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	0.0	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV- 3	1.0	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	0.0	Colon Pool	3.3
Ovarian ca. OVCAR-5	0.0	Small Intestine Pool	0.9
Ovarian ca. IGROV- 1	0.0	Stomach Pool	0.0
Ovarian ca. OVCAR-8	4.8	Bone Marrow Pool	0.0
Ovary	0.0	Fetal Heart	0.0
Breast ca. MCF-7	0.0	Heart Pool	0.0
Breast ca. MDA- MB-231	0.0	Lymph Node Pool	0.0
Breast ca. BT 549	0.0	Fetal Skeletal Muscle	0.0
Breast ca. T47D	4.9	Skeletal Muscle Pool	0.0
Breast ca. MDA-N	1.1	Spleen Pool	0.0
Breast Pool	2.2	Thymus Pool	0.7
Trachea	0.0	CNS cancer (glio/astro) U87-MG	0.0
Lung	0.0	CNS cancer (glio/astro) U-118-MG	20.4
Fetal Lung	0.0	CNS cancer (neuro;met) SK-N-AS	0.0

Lung ca. NCI-N417	0.0	CNS cancer (astro) SF-539	0.0
Lung ca. LX-1	0.0	CNS cancer (astro) SNB-75	0.0
Lung ca. NCI-H146	2.0	CNS cancer (glio) SNB-19	0.0
Lung ca. SHP-77	0.7	CNS cancer (glio) SF-295	100.0
Lung ca. A549	0.6	Brain (Amygdala) Pool	1.1
Lung ca. NCI-H526	0.0	Brain (cerebellum)	0.0
Lung ca. NCI-H23	0.0	Brain (fetal)	0.0
Lung ca. NCI-H460	0.0	Brain (Hippocampus) Pool	0.0
Lung ca. HOP-62	2.6	Cerebral Cortex Pool	0.0
Lung ca. NCI-H522	0.0	Brain (Substantia nigra) Pool	0.8
Liver	0.0	Brain (Thalamus) Pool	1.1
Fetal Liver	0.0	Brain (whole)	0.0
Liver ca. HepG2	0.0	Spinal Cord Pool	0.8
Kidney Pool	0.0	Adrenal Gland	2.0
Fetal Kidney	3.2	Pituitary gland Pool	0.0
Renal ca. 786-0	0.0	Salivary Gland	0.0
Renal ca. A498	0.0	Thyroid (female)	0.0
Renal ca. ACHN	0.0	Pancreatic ca. CAPAN2	0.0
Renal ca. UO-31	0.0	Pancreas Pool	1.8

Table BRC. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3464, Run 166417099	Tissue Name	Rel. Exp.(%) Ag3464, Run 166417099
Secondary Th1 act	0.0	HUVEC IL-1beta	0.0
Secondary Th2 act	0.0	HUVEC IFN gamma	0.0
Secondary Tr1 act	2.5	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	0.0	HUVEC IL-11	0.0
Secondary Tr1 rest	0.0	Lung Microvascular EC none	0.0
Primary Th1 act	0.0	Lung Microvascular EC TNFalpha + IL-1beta	0.0
Primary Th2 act	0.0	Microvascular Dermal EC none	0.0
Primary Tr1 act	0.0	Microvascular Dermal EC	0.0

		TNFalpha + IL-1beta	
Primary Th1 rest	0.0	Bronchial epithelium TNFalpha + IL1beta	0.0
Primary Th2 rest	0.0	Small airway epithelium none	0.0
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	0.0
CD45RA CD4 lymphocyte act	0.0	Coronary artery SMC rest	0.0
CD45RO CD4 lymphocyte act	0.0	Coronary artery SMC TNFalpha + IL-1beta	0.0
CD8 lymphocyte act	0.0	Astrocytes rest	0.0
Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFalpha + IL-1beta	0.0
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	12.0
2ry Th1/Th2/Tr1 _anti- CD95 CH11	5.9	CCD1106 (Keratinocytes) none	0.0
LAK cells rest	0.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0
LAK cells IL-2	0.0	Liver cirrhosis	100.0
LAK cells IL-2+IL-12	0.0	Lupus kidney	0.0
LAK cells IL-2+IFN gamma	0.0	NCI-H292 none	0.0
LAK cells IL-2+ IL-18	0.0	NCI-H292 IL-4	0.0
LAK cells PMA/ionomycin	0.0	NCI-H292 IL-9	10.0
NK Cells IL-2 rest	0.0	NCI-H292 IL-13	0.0
Two Way MLR 3 day	0.0	NCI-H292 IFN gamma	3.2
Two Way MLR 5 day	0.0	HPAEC none	0.0
Two Way MLR 7 day	0.0	HPAEC TNF alpha + IL-1 beta	0.0
PBMC rest	0.0	Lung fibroblast none	7.0
PBMC PWM	0.0	Lung fibroblast TNF alpha + IL-1 beta	0.0
PBMC PHA-L	0.0	Lung fibroblast IL-4	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-9	0.0
Ramos (B cell) ionomycin	0.0	Lung fibroblast IL-13	0.0
B lymphocytes PWM	0.0	Lung fibroblast IFN gamma	0.0
B lymphocytes CD40L and IL-4	0.0	Dermal fibroblast CCD1070 rest	0.0

EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 TNF alpha	0.0
EOL-1 dbcAMP PMA/ionomycin	0.0	Dermal fibroblast CCD1070 IL-1 beta	0.0
Dendritic cells none	0.0	Dermal fibroblast IFN gamma	0.0
Dendritic cells LPS	0.0	Dermal fibroblast IL-4	0.0
Dendritic cells anti- CD40	0.0	IBD Colitis 2	0.0
Monocytes rest	0.0	IBD Crohn's	6.3
Monocytes LPS	0.0	Colon	27.4
Macrophages rest	0.0	Lung	3.8
Macrophages LPS	0.0	Thymus	0.0
HUVEC none	0.0	Kidney	0.0
HUVEC starved	0.0		

CNS_neurodegeneration_v1.0 Summary: Ag3464 Expression of the CG59549-01 gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.4 Summary: Ag3464 Expression of the CG59549-01 gene is highest in a CNS cancer (glio) SF-295 sample (CT = 31.15). Thus, the expression of this gene could be used to distinguish this sample from the other samples in the panel. In addition, low to moderate expression of this gene is detected in a melanoma and a CNS cancer sample. Therefore, therapeutic modulation of this gene or its protein product may be beneficial in the treatment of melanoma and CNS cancer.

Panel 4D Summary: Ag3464 Low but significant expression of the CG59549-01 gene is detected exclusively in liver cirrhosis sample (CT=33.4). Therefore, expression of this gene may be used to distinguish liver cirrhosis from the other samples on this panel. Furthermore, expression of this gene is not detected in normal liver in Panel 1.3D, suggesting that its expression is unique to liver cirrhosis. Therefore, antibodies or small molecule therapeutics could reduce or inhibit fibrosis that occurs in liver cirrhosis. In addition, antibodies to this gene product could also be used for the diagnosis of liver cirrhosis.

BS. CG59641-01: ACETYL-COA CARBOXYLASE 2

Expression of gene CG59641-01 was assessed using the primer-probe set Ag3502, described in Table BSA. Results of the RTQ-PCR runs are shown in Table BSB.

Table BSA. Probe Name Ag3502

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-ctccctacgtcaccaaggat-3'	20	5090	614
Probe	TET-5'-aagcgattccaggccccagaccct-3'- TAMRA	23	5122	615
Reverse	5'-ccgggaagtcatagatgtaggt-3'	22	5152	616

Table BSB. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3502, Run 217131537	Tissue Name	Rel. Exp.(%) Ag3502, Run 217131537
Adipose	100.0	Renal ca. TK-10	6.6
Melanoma* Hs688(A).T	1.5	Bladder	14.2
Melanoma* Hs688(B).T	1.4	Gastric ca. (liver met.) NCI-N87	11.6
Melanoma* M14	7.2	Gastric ca. KATO III	4.2
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.5
Melanoma* SK- MEL-5	14.8	Colon ca. SW480	7.8
Squamous cell carcinoma SCC-4	0.2	Colon ca.* (SW480 met) SW620	5.8
Testis Pool	10.0	Colon ca. HT29	1.0
Prostate ca.* (bone met) PC-3	19.9	Colon ca. HCT-116	5.8
Prostate Pool	12.9	Colon ca. CaCo-2	8.2
Placenta	1.9	Colon cancer tissue	7.6
Uterus Pool	9.2	Colon ca. SW1116	2.0
Ovarian ca. OVCAR-3	6.6	Colon ca. Colo-205	9.0
Ovarian ca. SK-OV- 3	12.2	Colon ca. SW-48	1.7
Ovarian ca. OVCAR-4	1.9	Colon Pool	20.7
Ovarian ca. OVCAR-5	8.5	Small Intestine Pool	27.9
Ovarian ca. IGROV- 1	1.2	Stomach Pool	28.7
Ovarian ca. OVCAR-8	1.7	Bone Marrow Pool	8.0
Ovary	12.1	Fetal Heart	30.6
Breast ca. MCF-7	63.7	Heart Pool	16.7
Breast ca. MDA- MB-231	4.5	Lymph Node Pool	18.8

Breast ca. BT 549	1.8	Fetal Skeletal Muscle	5.4
Breast ca. T47D	10.8	Skeletal Muscle Pool	66.0
Breast ca. MDA-N	2.3	Spleen Pool	14.9
Breast Pool	39.0	Thymus Pool	16.4
Trachea	15.3	CNS cancer (glio/astro) U87-MG	5.8
Lung	5.6	CNS cancer (glio/astro) U-118-MG	9.1
Fetal Lung	13.6	CNS cancer (neuro;met) SK-N-AS	5.0
Lung ca. NCI-N417	2.3	CNS cancer (astro) SF- 539	3.1
Lung ca. LX-1	6.4	CNS cancer (astro) SNB-75	3.7
Lung ca. NCI-H146	2.2	CNS cancer (glio) SNB-19	1.3
Lung ca. SHP-77	2.8	CNS cancer (glio) SF- 295	8.1
Lung ca. A549	10.0	Brain (Amygdala) Pool	6.2
Lung ca. NCI-H526	0.9	Brain (cerebellum)	13.0
Lung ca. NCI-H23	26.6	Brain (fetal)	4.2
Lung ca. NCI-H460	3.9	Brain (Hippocampus) Pool	7.5
Lung ca. HOP-62	1.4	Cerebral Cortex Pool	8.4
Lung ca. NCI-H522	13.5	Brain (Substantia nigra) Pool	7.0
Liver	23.2	Brain (Thalamus) Pool	10.2
Fetal Liver	11.7	Brain (whole)	8.8
Liver ca. HepG2	6.6	Spinal Cord Pool	9.1
Kidney Pool	38.7	Adrenal Gland	50.0
Fetal Kidney	10.4	Pituitary gland Pool	7.4
Renal ca. 786-0	1.5	Salivary Gland	11.3
Renal ca. A498	1.4	Thyroid (female)	5.1
Renal ca. ACHN	3.0	Pancreatic ca. CAPAN2	1.7
Renal ca. UO-31	2.5	Pancreas Pool	17.0

General_screening_panel_v1.4 Summary: Ag3502 The CG59641-01 encodes an acetyl-CoA carboxylase 2 (ACC2) protein. Expression of this gene is highest in adipose tissue (CT=25.5). High levels of expression of this gene are also detected in other tissues with metabolic or endocrine function such as pancreas, adrenal gland, gastrointestinal tract, heart, skeletal muscle, and thyroid. Acetyl-coenzyme A (acetyl-CoA) carboxylase (ACC) catalyzes the synthesis of malonyl-CoA, a metabolite that plays a pivotal role in the synthesis and

oxidation of fatty. Hence, ACC links fatty acid and carbohydrate metabolism through the shared intermediate acetyl-CoA, the product of pyruvate dehydrogenase. It has been shown recently that mutations in ACC2 gene lead to loss of body fat in a normal caloric intake in mouse (Abu-Elheiga et al., 2001). Therefore, therapeutic modulation of the activity of this gene may prove useful in the treatment of endocrine/metabolically related diseases, such as obesity and diabetes.

Low to moderate expression of this gene is also detected in most of the samples used in this panel suggesting the possibility of a wider role in intercellular signaling for this molecule.

Among tissues that originate in the central nervous system, this gene is expressed in all regions represented on this panel. Therefore, therapeutic modulation of the expression or function of this gene may be useful in the treatment of neurologic disorders, such as Alzheimer's disease, Parkinson's disease, schizophrenia, multiple sclerosis, stroke and epilepsy.

In addition, significantly higher levels of expression are seen in a breast cancer cell line. Thus, expression of this gene could be used to differentiate between this sample and other samples on this panel and as a marker to detect the presence of breast cancer. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of breast cancer.

Reference:

1. Abu-Elheiga L, Matzuk MM, Abo-Hashema KA, Wakil SJ. (2001) Continuous fatty acid oxidation and reduced fat storage in mice lacking acetyl-CoA carboxylase 2. *Science* 2001 Mar 30;291(5513):2613-6

BT. CG59630-01: Midnolin

Expression of gene CG59630-01 was assessed using the primer-probe set Ag3425, described in Table BTA. Results of the RTQ-PCR runs are shown in Tables BTB, BTC and BTD.

Table BTA. Probe Name Ag3425

Primers	Sequences	Length	Start Position	SEQ ID
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				NO:
Forward	5'-aagctgaccttggtacccac-3'	20	295	617
Probe	TET-5'-ctcatgtctcaggcctcaaggcc-3'-TAMRA	23	328	618
Reverse	5'-ctctcgagagcttgcatcac-3'	20	361	619

Table BTB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3425, Run 210350911	Tissue Name	Rel. Exp.(%) Ag3425, Run 210350911
AD 1 Hippo	18.6	Control (Path) 3 Temporal Ctx	14.0
AD 2 Hippo	44.1	Control (Path) 4 Temporal Ctx	25.0
AD 3 Hippo	11.3	AD 1 Occipital Ctx	13.6
AD 4 Hippo	19.3	AD 2 Occipital Ctx (Missing)	0.0
AD 5 Hippo	53.2	AD 3 Occipital Ctx	11.5
AD 6 Hippo	100.0	AD 4 Occipital Ctx	24.7
Control 2 Hippo	47.0	AD 5 Occipital Ctx	53.2
Control 4 Hippo	38.2	AD 6 Occipital Ctx	80.7
Control (Path) 3 Hippo	10.5	Control 1 Occipital Ctx	19.9
AD 1 Temporal Ctx	17.3	Control 2 Occipital Ctx	49.3
AD 2 Temporal Ctx	33.7	Control 3 Occipital Ctx	31.2
AD 3 Temporal Ctx	10.4	Control 4 Occipital Ctx	13.9
AD 4 Temporal Ctx	19.1	Control (Path) 1 Occipital Ctx	81.2
AD 5 Inf Temporal Ctx	49.3	Control (Path) 2 Occipital Ctx	11.0
AD 5 Sup Temporal Ctx	45.4	Control (Path) 3 Occipital Ctx	8.4
AD 6 Inf Temporal Ctx	97.3	Control (Path) 4 Occipital Ctx	19.6
AD 6 Sup Temporal Ctx	85.9	Control 1 Parietal Ctx	18.8
Control 1 Temporal Ctx	20.3	Control 2 Parietal Ctx	29.9
Control 2 Temporal Ctx	59.9	Control 3 Parietal Ctx	32.3
Control 3 Temporal Ctx	32.3	Control (Path) 1 Parietal Ctx	91.4

Control 3 Temporal Ctx	17.4	Control (Path) 2 Parietal Ctx	32.3
Control (Path) 1 Temporal Ctx	70.7	Control (Path) 3 Parietal Ctx	7.7
Control (Path) 2 Temporal Ctx	27.5	Control (Path) 4 Parietal Ctx	45.1

Table BTC. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3425, Run 217049295	Tissue Name	Rel. Exp.(%) Ag3425, Run 217049295
Adipose	17.8	Renal ca. TK-10	26.4
Melanoma* Hs688(A).T	15.5	Bladder	16.0
Melanoma* Hs688(B).T	19.5	Gastric ca. (liver met.) NCI-N87	26.6
Melanoma* M14	10.5	Gastric ca. KATO III	23.0
Melanoma* LOXIMVI	15.7	Colon ca. SW-948	11.6
Melanoma* SK-MEL-5	8.0	Colon ca. SW480	27.5
Squamous cell carcinoma SCC-4	27.2	Colon ca.* (SW480 met) SW620	15.3
Testis Pool	5.6	Colon ca. HT29	15.2
Prostate ca.* (bone met) PC-3	18.7	Colon ca. HCT-116	40.6
Prostate Pool	3.3	Colon ca. CaCo-2	41.8
Placenta	16.8	Colon cancer tissue	19.6
Uterus Pool	2.6	Colon ca. SW1116	9.5
Ovarian ca. OVCAR-3	27.7	Colon ca. Colo-205	41.5
Ovarian ca. SK-OV-3	58.2	Colon ca. SW-48	6.8
Ovarian ca. OVCAR-4	4.0	Colon Pool	5.9
Ovarian ca. OVCAR-5	27.2	Small Intestine Pool	6.6
Ovarian ca. IGROV-1	30.1	Stomach Pool	42.9
Ovarian ca. OVCAR-8	19.3	Bone Marrow Pool	2.7
Ovary	7.6	Fetal Heart	9.0
Breast ca. MCF-7	37.1	Heart Pool	5.7
Breast ca. MDA-MB-231	15.3	Lymph Node Pool	6.5

Breast ca. BT 549	51.1	Fetal Skeletal Muscle	6.6
Breast ca. T47D	100.0	Skeletal Muscle Pool	17.4
Breast ca. MDA-N	8.3	Spleen Pool	11.2
Breast Pool	41.8	Thymus Pool	8.0
Trachea	15.9	CNS cancer (glio/astro) U87-MG	46.3
Lung	2.6	CNS cancer (glio/astro) U-118-MG	20.7
Fetal Lung	55.5	CNS cancer (neuro;met) SK-N-AS	29.1
Lung ca. NCI-N417	43.5	CNS cancer (astro) SF- 539	13.8
Lung ca. LX-1	23.5	CNS cancer (astro) SNB-75	36.9
Lung ca. NCI-H146	5.8	CNS cancer (glio) SNB-19	29.1
Lung ca. SHP-77	11.7	CNS cancer (glio) SF- 295	73.7
Lung ca. A549	21.5	Brain (Amygdala) Pool	5.3
Lung ca. NCI-H526	15.7	Brain (cerebellum)	14.6
Lung ca. NCI-H23	12.9	Brain (fetal)	20.6
Lung ca. NCI-H460	49.3	Brain (Hippocampus) Pool	4.6
Lung ca. HOP-62	10.1	Cerebral Cortex Pool	4.9
Lung ca. NCI-H522	16.2	Brain (Substantia nigra) Pool	10.4
Liver	1.3	Brain (Thalamus) Pool	6.1
Fetal Liver	9.3	Brain (whole)	45.1
Liver ca. HepG2	29.7	Spinal Cord Pool	5.8
Kidney Pool	8.0	Adrenal Gland	13.6
Fetal Kidney	11.3	Pituitary gland Pool	6.8
Renal ca. 786-0	23.0	Salivary Gland	4.6
Renal ca. A498	18.2	Thyroid (female)	13.9
Renal ca. ACHN	13.6	Pancreatic ca. CAPAN2	7.6
Renal ca. UO-31	28.5	Pancreas Pool	14.0

Table BTD. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag3425, Run 169839020	Tissue Name	Rel. Exp.(%) Ag3425, Run 169839020
Secondary Th1 act	20.6	HUVEC IL-1beta	46.7
Secondary Th2 act	30.6	HUVEC IFN gamma	23.3

Secondary Tr1 act	32.1	HUVEC TNF alpha + IFN gamma	13.3
Secondary Th1 rest	18.2	HUVEC TNF alpha + IL4	22.8
Secondary Th2 rest	23.8	HUVEC IL-11	22.5
Secondary Tr1 rest	12.6	Lung Microvascular EC none	37.9
Primary Th1 act	2.8	Lung Microvascular EC TNFalpha + IL-1beta	22.2
Primary Th2 act	24.7	Microvascular Dermal EC none	24.1
Primary Tr1 act	20.0	Microvascular Dermal EC TNFalpha + IL-1beta	21.2
Primary Th1 rest	18.6	Bronchial epithelium TNFalpha + IL1beta	26.6
Primary Th2 rest	19.5	Small airway epithelium none	23.5
Primary Tr1 rest	22.4	Small airway epithelium TNFalpha + IL-1beta	27.2
CD45RA CD4 lymphocyte act	17.7	Coronary artery SMC rest	22.1
CD45RO CD4 lymphocyte act	19.8	Coronary artery SMC TNFalpha + IL-1beta	20.2
CD8 lymphocyte act	14.1	Astrocytes rest	24.7
Secondary CD8 lymphocyte rest	23.8	Astrocytes TNFalpha + IL-1beta	17.8
Secondary CD8 lymphocyte act	12.2	KU-812 (Basophil) rest	16.5
CD4 lymphocyte none	6.5	KU-812 (Basophil) PMA/ionomycin	36.6
2ry Th1/Th2/Tr1_anti-CD95 CH11	15.2	CCD1106 (Keratinocytes) none	40.1
LAK cells rest	34.2	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	41.8
LAK cells IL-2	24.5	Liver cirrhosis	20.0
LAK cells IL-2+IL-12	21.6	NCI-H292 none	41.2
LAK cells IL-2+IFN gamma	23.2	NCI-H292 IL-4	58.6
LAK cells IL-2+ IL-18	22.2	NCI-H292 IL-9	61.6
LAK cells PMA/ionomycin	97.3	NCI-H292 IL-13	47.6
NK Cells IL-2 rest	28.7	NCI-H292 IFN gamma	54.0
Two Way MLR 3 day	32.5	HPAEC none	16.6
Two Way MLR 5 day	30.1	HPAEC TNF alpha + IL-1 beta	20.7
Two Way MLR 7 day	18.7	Lung fibroblast none	46.0

PBMC rest	27.9	Lung fibroblast TNF alpha + IL-1 beta	20.2
PBMC PWM	25.3	Lung fibroblast IL-4	47.0
PBMC PHA-L	22.7	Lung fibroblast IL-9	52.1
Ramos (B cell) none	25.5	Lung fibroblast IL-13	45.1
Ramos (B cell) ionomycin	23.5	Lung fibroblast IFN gamma	50.0
B lymphocytes PWM	17.8	Dermal fibroblast CCD1070 rest	28.3
B lymphocytes CD40L and IL-4	23.8	Dermal fibroblast CCD1070 TNF alpha	37.1
EOL-1 dbcAMP	34.4	Dermal fibroblast CCD1070 IL-1 beta	13.3
EOL-1 dbcAMP PMA/ionomycin	87.7	Dermal fibroblast IFN gamma	28.5
Dendritic cells none	32.3	Dermal fibroblast IL-4	26.2
Dendritic cells LPS	21.5	Dermal Fibroblasts rest	26.6
Dendritic cells anti-CD40	32.8	Neutrophils TNFa+LPS	33.7
Monocytes rest	54.3	Neutrophils rest	100.0
Monocytes LPS	93.3	Colon	18.4
Macrophages rest	23.8	Lung	28.7
Macrophages LPS	36.1	Thymus	28.1
HUVEC none	24.7	Kidney	14.0
HUVEC starved	38.4		

CNS_neurodegeneration_v1.0 Summary: Ag3425 This panel confirms the expression of this gene at low levels in the brain in an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. Please see Panel 1.4 for a discussion of the potential utility of this gene in treatment of central nervous system disorders.

General_screening_panel_v1.4 Summary: Ag3425 The CG59630-01 gene is a homologue of mouse midnoline (midbrain nucleolar protein). Its expression is moderate to high across all of the samples on this panel, with highest expression in a breast cancer cell line (CT=25.3). The widespread expression suggests that this gene may play an important role in cellular function. In mouse, the expression of this gene is developmentally regulated: it is strongly expressed at the mesencephalon (midbrain) of the embryo and is involved in regulation of genes related to neurogenesis in the nucleolus (Tsukahara et al., 2000). Based on the gene's expression in all CNS regions examined, this gene may therefore play a role in central nervous

system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

Among tissues with metabolic function, this gene is expressed at moderate to low levels in pituitary, adipose, adrenal gland, pancreas, thyroid, and adult and fetal skeletal muscle, heart, and liver. This widespread expression among these tissues suggests that this gene product may play a role in normal neuroendocrine and metabolic and that dysregulated expression of this gene may contribute to neuroendocrine disorders or metabolic diseases, such as obesity and diabetes.

Reference:

1. Tsukahara M, Suemori H, Noguchi S, Ji ZS, Tsunoo H. (2000) Novel nucleolar protein, midnolin, is expressed in the mesencephalon during mouse development. *Gene* 2000 Aug 22;254(1-2):45-55

Panel 4.1D Summary: Ag3425 The CG59630-01 gene is a homologue of mouse midnoline (midbrain nucleolar protein). Its expression is moderate to high across all of the samples on this panel, with highest expression in resting neutrophils (CT=29.1). In addition, this gene is expressed at high to moderate levels in a wide range of cell types of significance in the immune response in health and disease. These cells include members of the T-cell, B-cell, endothelial cell, macrophage/monocyte, and peripheral blood mononuclear cell family, as well as epithelial and fibroblast cell types from lung and skin, and normal tissues represented by colon, lung, thymus and kidney. This ubiquitous pattern of expression suggests that this gene product may be involved in homeostatic processes for these and other cell types and tissues. This pattern is in agreement with the expression profile in General_screening_panel_v1.4 and also suggests a role for the gene product in cell survival and proliferation. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

BU. CG59561-01: CYTOSOLIC ACYL COENZYME A THIOESTER HYDROLASE

Expression of gene CG59561-01 was assessed using the primer-probe set Ag3424, described in Table BUA. Results of the RTQ-PCR runs are shown in Tables BUB, BUC and BUD.

Table BUA. Probe Name Ag3424

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5' -aagctgaccaataaggccac-3'	20	345	620
Probe	TET-5' -gtggacaaggtcctcgaagagcctc-3' - TAMRA	25	396	621
Reverse	5' -ctgccggaaatacacacacag-3'	20	421	622

Table BUB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3424, Run 210350585	Tissue Name	Rel. Exp.(%) Ag3424, Run 210350585
AD 1 Hippo	8.8	Control (Path) 3 Temporal Ctx	1.5
AD 2 Hippo	16.7	Control (Path) 4 Temporal Ctx	25.5
AD 3 Hippo	2.7	AD 1 Occipital Ctx	3.7
AD 4 Hippo	4.7	AD 2 Occipital Ctx (Missing)	0.0
AD 5 hippo	100.0	AD 3 Occipital Ctx	2.0
AD 6 Hippo	34.6	AD 4 Occipital Ctx	8.5
Control 2 Hippo	44.8	AD 5 Occipital Ctx	11.7
Control 4 Hippo	2.2	AD 6 Occipital Ctx	90.8
Control (Path) 3 Hippo	2.0	Control 1 Occipital Ctx	0.8
AD 1 Temporal Ctx	2.4	Control 2 Occipital Ctx	84.1
AD 2 Temporal Ctx	16.6	Control 3 Occipital Ctx	5.1
AD 3 Temporal Ctx	2.1	Control 4 Occipital Ctx	1.3
AD 4 Temporal Ctx	8.6	Control (Path) 1 Occipital Ctx	96.6
AD 5 Inf Temporal Ctx	62.9	Control (Path) 2 Occipital Ctx	5.7
AD 5 SupTemporal Ctx	28.3	Control (Path) 3 Occipital Ctx	0.5
AD 6 Inf Temporal Ctx	26.6	Control (Path) 4 Occipital Ctx	8.8

AD 6 Sup Temporal Ctx	22.1	Control 1 Parietal Ctx	2.0
Control 1 Temporal Ctx	1.2	Control 2 Parietal Ctx	22.1
Control 2 Temporal Ctx	65.1	Control 3 Parietal Ctx	19.9
Control 3 Temporal Ctx	8.7	Control (Path) 1 Parietal Ctx	94.0
Control 4 Temporal Ctx	2.4	Control (Path) 2 Parietal Ctx	14.0
Control (Path) 1 Temporal Ctx	61.1	Control (Path) 3 Parietal Ctx	0.9
Control (Path) 2 Temporal Ctx	28.3	Control (Path) 4 Parietal Ctx	39.0

Table BUC. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3424, Run 166385382	Tissue Name	Rel. Exp.(%) Ag3424, Run 166385382
Secondary Th1 act	62.9	HUVEC IL-1beta	4.0
Secondary Th2 act	37.9	HUVEC IFN gamma	10.7
Secondary Tr1 act	68.8	HUVEC TNF alpha + IFN gamma	18.6
Secondary Th1 rest	4.2	HUVEC TNF alpha + IL4	15.5
Secondary Th2 rest	12.1	HUVEC IL-11	10.2
Secondary Tr1 rest	4.4	Lung Microvascular EC none	28.7
Primary Th1 act	66.9	Lung Microvascular EC TNFalpha + IL-1beta	25.7
Primary Th2 act	61.1	Microvascular Dermal EC none	36.3
Primary Tr1 act	43.2	Microvascular Dermal EC TNFalpha + IL-1beta	20.3
Primary Th1 rest	30.1	Bronchial epithelium TNFalpha + IL1beta	25.5
Primary Th2 rest	17.4	Small airway epithelium none	19.5
Primary Tr1 rest	15.9	Small airway epithelium TNFalpha + IL-1beta	52.1
CD45RA CD4 lymphocyte act	14.8	Coronary artery SMC rest	14.8
CD45RO CD4 lymphocyte act	37.6	Coronary artery SMC TNFalpha + IL-1beta	8.3
CD8 lymphocyte act	43.8	Astrocytes rest	13.9

Secondary CD8 lymphocyte rest	49.7	Astrocytes TNFalpha + IL-1beta	13.3
Secondary CD8 lymphocyte act	24.1	KU-812 (Basophil) rest	23.8
CD4 lymphocyte none	0.9	KU-812 (Basophil) PMA/ionomycin	51.4
2ry Th1/Th2/Tr1_anti-CD95 CH11	9.0	CCD1106 (Keratinocytes) none	62.4
LAK cells rest	33.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	37.1
LAK cells IL-2	27.7	Liver cirrhosis	3.5
LAK cells IL-2+IL-12	25.5	Lupus kidney	1.0
LAK cells IL-2+IFN gamma	35.6	NCI-H292 none	16.2
LAK cells IL-2+ IL-18	21.9	NCI-H292 IL-4	23.5
LAK cells PMA/ionomycin	3.6	NCI-H292 IL-9	29.5
NK Cells IL-2 rest	15.1	NCI-H292 IL-13	13.4
Two Way MLR 3 day	9.4	NCI-H292 IFN gamma	20.6
Two Way MLR 5 day	17.4	HPAEC none	17.4
Two Way MLR 7 day	13.1	HPAEC TNF alpha + IL-1 beta	20.9
PBMC rest	0.8	Lung fibroblast none	37.9
PBMC PWM	88.9	Lung fibroblast TNF alpha + IL-1 beta	34.9
PBMC PHA-L	52.5	Lung fibroblast IL-4	69.7
Ramos (B cell) none	17.2	Lung fibroblast IL-9	49.7
Ramos (B cell) ionomycin	31.9	Lung fibroblast IL-13	45.4
B lymphocytes PWM	75.8	Lung fibroblast IFN gamma	90.8
B lymphocytes CD40L and IL-4	9.9	Dermal fibroblast CCD1070 rest	54.3
EOL-1 dbcAMP	11.0	Dermal fibroblast CCD1070 TNF alpha	84.1
EOL-1 dbcAMP PMA/ionomycin	8.1	Dermal fibroblast CCD1070 IL-1 beta	30.6
Dendritic cells none	38.2	Dermal fibroblast IFN gamma	31.4
Dendritic cells LPS	31.9	Dermal fibroblast IL-4	45.4
Dendritic cells anti-CD40	37.1	IBD Colitis 2	2.5
Monocytes rest	0.4	IBD Crohn's	4.7
Monocytes LPS	0.6	Colon	45.4

Macrophages rest	12.6	Lung	16.6
Macrophages LPS	5.8	Thymus	100.0
HUVEC none	16.0	Kidney	20.6
HUVEC starved	27.4		

Table BUD. Panel 5 Islet

Tissue Name	Rel. Exp.(%) Ag3424, Run 242385366	Tissue Name	Rel. Exp.(%) Ag3424, Run 242385366
97457_Patient-02go_adipose	8.2	94709_Donor 2 AM - A_adipose	6.7
97476_Patient-07sk_skeletal muscle	3.9	94710_Donor 2 AM - B_adipose	8.7
97477_Patient-07ut_uterus	7.4	94711_Donor 2 AM - C_adipose	5.9
97478_Patient-07pl_placenta	7.9	94712_Donor 2 AD - A_adipose	8.3
99167_Bayer Patient 1	4.8	94713_Donor 2 AD - B_adipose	5.4
97482_Patient-08ut_uterus	4.1	94714_Donor 2 AD - C_adipose	7.7
97483_Patient-08pl_placenta	2.4	94742_Donor 3 U - A_Mesenchymal Stem Cells	3.0
97486_Patient-09sk_skeletal muscle	0.0	94743_Donor 3 U - B_Mesenchymal Stem Cells	9.9
97487_Patient-09ut_uterus	5.3	94730_Donor 3 AM - A_adipose	22.5
97488_Patient-09pl_placenta	2.3	94731_Donor 3 AM - B_adipose	15.1
97492_Patient-10ut_uterus	4.8	94732_Donor 3 AM - C_adipose	10.2
97493_Patient-10pl_placenta	6.6	94733_Donor 3 AD - A_adipose	29.7
97495_Patient-11go_adipose	0.9	94734_Donor 3 AD - B_adipose	6.4
97496_Patient-11sk_skeletal muscle	0.3	94735_Donor 3 AD - C_adipose	34.9
97497_Patient-11ut_uterus	9.8	77138_Liver_HepG2untreated	57.8
97498_Patient-11pl_placenta	3.0	73556_Heart_Cardiac stromal cells (primary)	10.3
97500_Patient-12go_adipose	1.7	81735_Small Intestine	23.7
97501_Patient-12sk_skeletal muscle	1.4	72409_Kidney_Proximal Convoluted Tubule	4.5

97502_Patient-12ut_uterus	10.2	82685_Small intestine_Duodenum	1.2
97503_Patient-12pl_placenta	3.2	90650_Adrenal_Adrenocortical adenoma	1.4
94721_Donor 2 U - A_Mesenchymal Stem Cells	6.8	72410_Kidney_HRCE	100.0
94722_Donor 2 U - B_Mesenchymal Stem Cells	2.8	72411_Kidney_HRE	69.7
94723_Donor 2 U - C_Mesenchymal Stem Cells	5.1	73139_Uterus_Uterine smooth muscle cells	22.4

CNS_neurodegeneration_v1.0 Summary: Ag3424 This panel confirms the expression of the CG59561-01 gene at low levels in the brain in an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. This expression profile suggests that this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

General_screening_panel_v1.4 Summary: Ag3424 Results from one experiment with the CG59561-01 gene are not included. The amp plot indicates that there were experimental difficulties with this run. (Data not shown.)

Panel 4D Summary: Ag3424 The CG59561-01 gene encodes a protein homologous to cytosolic acyl coenzyme A thioester hydrolase (Brain acyl-CoA hydrolase, BACH). Among the tissue samples used in this panel, highest expression of this gene is detected in thymus (CT=29.6). In addition, expression of this gene is stimulated in activated primary and secondary - Th1, Th2 and Tr1 cells. Therefore, this gene product may play an important role in T cell development. Thus, therapeutics designed with the protein encoded for by this transcript could be important in regulating T cell function and treating T cell mediated diseases such as emphysema, asthma, arthritis, psoriasis, IBD, and systemic lupus erythematosus.

Interestingly, expression of this gene is also seen in activated PBMCs (CTs=30) as compared to resting PBMCs.(CT=36) suggesting a role for this gene product in B-cell and T-cell proliferation. Therefore, small molecules that antagonize the function of this gene product may be useful as therapeutic drugs to reduce or eliminate the symptoms in patients with

autoimmune and inflammatory diseases in which B cells play a part in the initiation or progression of the disease process, such as systemic lupus erythematosus, Crohn's disease, ulcerative colitis, multiple sclerosis, chronic obstructive pulmonary disease, asthma, emphysema, rheumatoid arthritis, or psoriasis.

Panel 5 Islet Summary: Ag3424 The CG59561-01 gene is expressed at low levels in adipose and placenta, with highest expression in the kidney (CT=30.8). As an enzyme involved in lipid homeostasis, therapeutic modulation of this gene product may be a treatment for obesity and obesity-related diseases, including Type 2 diabetes.

BV. CG59452-01: CELL PROLIFERATION RELATED PROTEIN CAP -

Expression of gene CG59452-01 was assessed using the primer-probe set Ag3443, described in Table BVA. Results of the RTQ-PCR runs are shown in Tables BVB and BVC.

Table BVA. Probe Name Ag3443

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5' -caggaatgtatccaggacttca-3'	22	387	623
Probe	TET-5' -catctacaacaagcctggagatgaca-3' - TAMRA	26	431	624
Reverse	5' -tttcagagcttctgccatt-3'	20	464	625

Table BVB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3443, Run 210374885	Tissue Name	Rel. Exp.(%) Ag3443, Run 210374885
AD 1 Hippo	10.2	Control (Path) 3 Temporal Ctx	6.2
AD 2 Hippo	28.3	Control (Path) 4 Temporal Ctx	27.0
AD 3 Hippo	8.0	AD 1 Occipital Ctx	13.6
AD 4 Hippo	4.8	AD 2 Occipital Ctx (Missing)	0.0
AD 5 Hippo	84.1	AD 3 Occipital Ctx	6.0
AD 6 Hippo	71.7	AD 4 Occipital Ctx	17.9
Control 2 Hippo	31.4	AD 5 Occipital Ctx	54.3
Control 4 Hippo	6.1	AD 6 Occipital Ctx	22.7
Control (Path) 3 Hippo	3.3	Control 1 Occipital Ctx	4.0
AD 1 Temporal Ctx	21.9	Control 2 Occipital	73.7

		Ctx	
AD 2 Temporal Ctx	33.4	Control 3 Occipital Ctx	13.7
AD 3 Temporal Ctx	7.4	Control 4 Occipital Ctx	7.7
AD 4 Temporal Ctx	16.8	Control (Path) 1 Occipital Ctx	100.0
AD 5 Inf Temporal Ctx	74.7	Control (Path) 2 Occipital Ctx	11.0
AD 5 Sup Temporal Ctx	36.1	Control (Path) 3 Occipital Ctx	1.3
AD 6 Inf Temporal Ctx	79.0	Control (Path) 4 Occipital Ctx	15.3
AD 6 Sup Temporal Ctx	85.9	Control 1 Parietal Ctx	6.1
Control 1 Temporal Ctx	8.6	Control 2 Parietal Ctx	35.8
Control 2 Temporal Ctx	48.3	Control 3 Parietal Ctx	12.9
Control 3 Temporal Ctx	11.4	Control (Path) 1 Parietal Ctx	59.5
Control 3 Temporal Ctx	6.5	Control (Path) 2 Parietal Ctx	25.5
Control (Path) 1 Temporal Ctx	93.3	Control (Path) 3 Parietal Ctx	2.4
Control (Path) 2 Temporal Ctx	23.8	Control (Path) 4 Parietal Ctx	23.2

Table BVC. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3443, Run 166397102	Tissue Name	Rel. Exp.(%) Ag3443, Run 166397102
Secondary Th1 act	22.7	HUVEC IL-1beta	18.2
Secondary Th2 act	25.7	HUVEC IFN gamma	18.6
Secondary Tr1 act	37.9	HUVEC TNF alpha + IFN gamma	16.6
Secondary Th1 rest	15.7	HUVEC TNF alpha + IL4	17.0
Secondary Th2 rest	11.2	HUVEC IL-11	9.3
Secondary Tr1 rest	11.5	Lung Microvascular EC none	14.2
Primary Th1 act	16.6	Lung Microvascular EC TNFalpha + IL-1beta	12.9
Primary Th2 act	29.9	Microvascular Dermal EC none	17.7

Primary Tr1 act	44.1	Microsvascular Dermal EC TNFalpha + IL-1beta	17.1
Primary Th1 rest	69.7	Bronchial epithelium TNFalpha + IL1beta	6.8
Primary Th2 rest	40.9	Small airway epithelium none	8.5
Primary Tr1 rest	24.5	Small airway epithelium TNFalpha + IL-1beta	40.9
CD45RA CD4 lymphocyte act	15.6	Coronary artery SMC rest	9.4
CD45RO CD4 lymphocyte act	30.4	Coronary artery SMC TNFalpha + IL-1beta	8.5
CD8 lymphocyte act	19.3	Astrocytes rest	16.3
Secondary CD8 lymphocyte rest	27.7	Astrocytes TNFalpha + IL-1beta	30.4
Secondary CD8 lymphocyte act	16.3	KU-812 (Basophil) rest	26.8
CD4 lymphocyte none	12.4	KU-812 (Basophil) PMA/ionomycin	80.7
2ry Th1/Th2/Tr1_anti- CD95 CH11	17.3	CCD1106 (Keratinocytes) none	13.6
LAK cells rest	10.7	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	100.0
LAK cells IL-2	30.4	Liver cirrhosis	10.4
LAK cells IL-2+IL-12	24.5	Lupus kidney	16.5
LAK cells IL-2+IFN gamma	34.2	NCI-H292 none	22.4
LAK cells IL-2+ IL-18	20.9	NCI-H292 IL-4	36.9
LAK cells PMA/ionomycin	13.3	NCI-H292 IL-9	27.5
NK Cells IL-2 rest	15.6	NCI-H292 IL-13	15.9
Two Way MLR 3 day	19.5	NCI-H292 IFN gamma	15.9
Two Way MLR 5 day	16.2	HPAEC none	9.3
Two Way MLR 7 day	15.1	HPAEC TNF alpha + IL-1 beta	18.9
PBMC rest	13.1	Lung fibroblast none	20.4
PBMC PWM	26.6	Lung fibroblast TNF alpha + IL-1 beta	20.9
PBMC PHA-L	9.6	Lung fibroblast IL-4	19.5
Ramos (B cell) none	39.2	Lung fibroblast IL-9	12.2
Ramos (B cell) ionomycin	37.9	Lung fibroblast IL-13	10.5
B lymphocytes PWM	31.4	Lung fibroblast IFN gamma	29.1
B lymphocytes CD40L	32.3	Dermal fibroblast	26.8

and IL-4		CCD1070 rest	
EOL-1 dbcAMP	18.7	Dermal fibroblast CCD1070 TNF alpha	46.3
EOL-1 dbcAMP PMA/ionomycin	45.7	Dermal fibroblast CCD1070 IL-1 beta	16.0
Dendritic cells none	12.8	Dermal fibroblast IFN gamma	7.5
Dendritic cells LPS	9.6	Dermal fibroblast IL-4	17.1
Dendritic cells anti- CD40	14.6	IBD Colitis 2	4.2
Monocytes rest	20.6	IBD Crohn's	2.9
Monocytes LPS	20.9	Colon	49.0
Macrophages rest	15.8	Lung	11.1
Macrophages LPS	12.9	Thymus	20.2
HUVEC none	24.3	Kidney	33.2
HUVEC starved	33.7		

CNS_neurodegeneration_v1.0 Summary: Ag3443 This panel confirms the expression of the CG59452-01 gene at significant levels in the brain in an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. Expression of this gene in the brain suggests that it may play a role in central nervous system disorders other than Alzheimer's disease, such as Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

General_screening_panel_v1.4 Summary: Ag3443 The amp plot indicates that there were experimental difficulties with this run. (Data not shown).

Panel 4D Summary: Ag3443 Highest expression of the CG59452-01 gene is detected in TNFalpha + IL-1beta treated keratinocytes and PMA/ionomycin treated KU-812 basophil cells (CTs=24.5). Thus, antibody or small molecule therapies designed with the protein encoded for by this gene could block or inhibit inflammation or tissue damage due to basophil activation in response to asthma, allergies, hypersensitivity reactions, psoriasis, and viral infections.

BW. CG59572-01 and CG59572-02: Pseudouridine Synthase 3

Expression of gene CG59572-01 and CG59572-02 was assessed using the primer-probe set Ag3476, described in Table BWA. Results of the RTQ-PCR runs are shown in

Tables BWB, BWC and BWD. Please note that CG59572-02 represents a full-length physical clone of the CG59572-01 gene, validating the prediction of the gene sequence.

Table BWA. Probe Name Ag3476

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-acctacaacaactgtgggctaa-3'	22	1070	626
Probe	TET-5'-tcattgtgtcaaaactcacatgttgt-3'- TAMRA	26	1092	627
Reverse	5'-ggaacagtgtccagtccttgta-3'	22	1127	628

Table BWB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3476, Run 210377171	Tissue Name	Rel. Exp.(%) Ag3476, Run 210377171
AD 1 Hippo	16.7	Control (Path) 3 Temporal Ctx	4.5
AD 2 Hippo	23.8	Control (Path) 4 Temporal Ctx	31.6
AD 3 Hippo	10.3	AD 1 Occipital Ctx	28.5
AD 4 Hippo	8.5	AD 2 Occipital Ctx (Missing)	0.0
AD 5 hippo	88.3	AD 3 Occipital Ctx	7.9
AD 6 Hippo	77.4	AD 4 Occipital Ctx	20.6
Control 2 Hippo	37.4	AD 5 Occipital Ctx	35.4
Control 4 Hippo	9.6	AD 6 Occipital Ctx	54.7
Control (Path) 3 Hippo	8.4	Control 1 Occipital Ctx	4.7
AD 1 Temporal Ctx	18.6	Control 2 Occipital Ctx	67.8
AD 2 Temporal Ctx	32.3	Control 3 Occipital Ctx	15.6
AD 3 Temporal Ctx	8.0	Control 4 Occipital Ctx	5.6
AD 4 Temporal Ctx	21.6	Control (Path) 1 Occipital Ctx	100.0
AD 5 Inf Temporal Ctx	84.1	Control (Path) 2 Occipital Ctx	7.8
AD 5 Sup Temporal Ctx	41.5	Control (Path) 3 Occipital Ctx	5.9
AD 6 Inf Temporal Ctx	77.4	Control (Path) 4 Occipital Ctx	18.0
AD 6 Sup Temporal	88.3	Control 1 Parietal	8.1

Ctx		Ctx	
Control 1 Temporal Ctx	5.4	Control 2 Parietal Ctx	47.0
Control 2 Temporal Ctx	40.1	Control 3 Parietal Ctx	18.2
Control 3 Temporal Ctx	22.1	Control (Path) 1 Parietal Ctx	71.7
Control 4 Temporal Ctx	5.1	Control (Path) 2 Parietal Ctx	20.6
Control (Path) 1 Temporal Ctx	55.1	Control (Path) 3 Parietal Ctx	5.3
Control (Path) 2 Temporal Ctx	31.6	Control (Path) 4 Parietal Ctx	46.3

Table BWC. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3476, Run 217119004	Tissue Name	Rel. Exp.(%) Ag3476, Run 217119004
Adipose	5.7	Renal ca. TK-10	13.9
Melanoma* Hs688(A).T	13.4	Bladder	16.3
Melanoma* Hs688(B).T	14.6	Gastric ca. (liver met.) NCI-N87	42.9
Melanoma* M14	18.6	Gastric ca. KATO III	92.0
Melanoma* LOXIMVI	38.7	Colon ca. SW-948	7.3
Melanoma* SK-MEL-5	27.0	Colon ca. SW480	40.9
Squamous cell carcinoma SCC-4	9.9	Colon ca.* (SW480 met) SW620	27.5
Testis Pool	5.9	Colon ca. HT29	24.0
Prostate ca.* (bone met) PC-3	34.4	Colon ca. HCT-116	32.5
Prostate Pool	5.6	Colon ca. CaCo-2	52.1
Placenta	1.1	Colon cancer tissue	10.4
Uterus Pool	3.8	Colon ca. SW1116	3.9
Ovarian ca. OVCAR-3	15.4	Colon ca. Colo-205	6.1
Ovarian ca. SK-OV-3	20.7	Colon ca. SW-48	9.0
Ovarian ca. OVCAR-4	14.5	Colon Pool	13.6
Ovarian ca. OVCAR-5	44.8	Small Intestine Pool	8.4
Ovarian ca. IGROV-	18.4	Stomach Pool	7.0

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Ovarian ca. OVCAR-8	10.3	Bone Marrow Pool	4.0
Ovary	7.0	Fetal Heart	6.3
Breast ca. MCF-7	16.8	Heart Pool	5.4
Breast ca. MDA-MB-231	31.0	Lymph Node Pool	14.5
Breast ca. BT 549	51.1	Fetal Skeletal Muscle	4.2
Breast ca. T47D	100.0	Skeletal Muscle Pool	10.7
Breast ca. MDA-N	28.7	Spleen Pool	5.4
Breast Pool	11.0	Thymus Pool	8.2
Trachea	6.2	CNS cancer (glio/astro) U87-MG	11.9
Lung	2.0	CNS cancer (glio/astro) U-118-MG	44.1
Fetal Lung	15.5	CNS cancer (neuro;met) SK-N-AS	29.9
Lung ca. NCI-N417	14.5	CNS cancer (astro) SF-539	13.6
Lung ca. LX-1	31.0	CNS cancer (astro) SNB-75	43.8
Lung ca. NCI-H146	9.3	CNS cancer (glio) SNB-19	16.0
Lung ca. SHP-77	36.6	CNS cancer (glio) SF-295	44.8
Lung ca. A549	14.4	Brain (Amygdala) Pool	3.6
Lung ca. NCI-H526	21.6	Brain (cerebellum)	7.8
Lung ca. NCI-H23	23.0	Brain (fetal)	7.6
Lung ca. NCI-H460	13.9	Brain (Hippocampus) Pool	4.5
Lung ca. HOP-62	14.9	Cerebral Cortex Pool	6.3
Lung ca. NCI-H522	38.7	Brain (Substantia nigra) Pool	3.4
Liver	1.9	Brain (Thalamus) Pool	6.9
Fetal Liver	17.2	Brain (whole)	3.8
Liver ca. HepG2	18.4	Spinal Cord Pool	3.6
Kidney Pool	12.9	Adrenal Gland	3.8
Fetal Kidney	15.3	Pituitary gland Pool	3.2
Renal ca. 786-0	13.4	Salivary Gland	1.8
Renal ca. A498	7.1	Thyroid (female)	4.4
Renal ca. ACHN	10.4	Pancreatic ca. CAPAN2	27.7
Renal ca. UO-31	22.1	Pancreas Pool	14.7

Table BWD. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3476, Run 166420471	Tissue Name	Rel. Exp.(%) Ag3476, Run 166420471
Secondary Th1 act	31.4	HUVEC IL-1beta	27.5
Secondary Th2 act	30.6	HUVEC IFN gamma	23.7
Secondary Tr1 act	40.3	HUVEC TNF alpha + IFN gamma	15.4
Secondary Th1 rest	11.6	HUVEC TNF alpha + IL4	16.2
Secondary Th2 rest	9.3	HUVEC IL-11	13.4
Secondary Tr1 rest	9.2	Lung Microvascular EC none	12.3
Primary Th1 act	23.5	Lung Microvascular EC TNFalpha + IL-1beta	11.0
Primary Th2 act	44.8	Microvascular Dermal EC none	20.3
Primary Tr1 act	55.5	Microvascular Dermal EC TNFalpha + IL-1beta	13.6
Primary Th1 rest	48.6	Bronchial epithelium TNFalpha + IL1beta	7.8
Primary Th2 rest	24.7	Small airway epithelium none	9.5
Primary Tr1 rest	22.8	Small airway epithelium TNFalpha + IL-1beta	48.0
CD45RA CD4 lymphocyte act	15.9	Coronary artery SMC rest	14.1
CD45RO CD4 lymphocyte act	45.1	Coronary artery SMC TNFalpha + IL-1beta	9.8
CD8 lymphocyte act	26.2	Astrocytes rest	13.9
Secondary CD8 lymphocyte rest	46.3	Astrocytes TNFalpha + IL-1beta	14.2
Secondary CD8 lymphocyte act	23.0	KU-812 (Basophil) rest	29.5
CD4 lymphocyte none	6.3	KU-812 (Basophil) PMA/ionomycin	55.1
2ry Th1/Th2/Tr1_anti- CD95 CH11	15.8	CCD1106 (Keratinocytes) none	18.7
LAK cells rest	8.4	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	100.0
LAK cells IL-2	29.1	Liver cirrhosis	12.8
LAK cells IL-2+IL-12	35.8	Lupus kidney	7.9
LAK cells IL-2+IFN gamma	42.6	NCI-H292 none	44.4
LAK cells IL-2+ IL-18	28.7	NCI-H292 IL-4	52.5
LAK cells PMA/ionomycin	14.0	NCI-H292 IL-9	55.5

NK Cells IL-2 rest	19.9	NCI-H292 IL-13	29.3
Two Way MLR 3 day	23.0	NCI-H292 IFN gamma	30.1
Two Way MLR 5 day	31.0	HPAEC none	10.7
Two Way MLR 7 day	18.0	HPAEC TNF alpha + IL-1 beta	13.1
PBMC rest	4.8	Lung fibroblast none	23.3
PBMC PWM	39.5	Lung fibroblast TNF alpha + IL-1 beta	16.0
PBMC PHA-L	11.4	Lung fibroblast IL-4	27.7
Ramos (B cell) none	18.2	Lung fibroblast IL-9	22.5
Ramos (B cell) ionomycin	16.2	Lung fibroblast IL-13	19.6
B lymphocytes PWM	56.3	Lung fibroblast IFN gamma	48.3
B lymphocytes CD40L and IL-4	36.9	Dermal fibroblast CCD1070 rest	28.5
EOL-1 dbcAMP	23.5	Dermal fibroblast CCD1070 TNF alpha	38.7
EOL-1 dbcAMP PMA/ionomycin	20.0	Dermal fibroblast CCD1070 IL-1 beta	11.8
Dendritic cells none	10.1	Dermal fibroblast IFN gamma	9.9
Dendritic cells LPS	9.7	Dermal fibroblast IL-4	15.7
Dendritic cells anti-CD40	10.2	IBD Colitis 2	6.6
Monocytes rest	12.0	IBD Crohn's	6.2
Monocytes LPS	12.5	Colon	46.0
Macrophages rest	13.3	Lung	12.6
Macrophages LPS	7.4	Thymus	21.8
HUVEC none	24.3	Kidney	18.3
HUVEC starved	33.4		

CNS_neurodegeneration_v1.0 Summary: Ag3476 This panel confirms the expression of the CG59572-01 gene at low levels in the brain in an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. Please see Panel 1.4 for a discussion of the potential utility of this gene in treatment of central nervous system disorders.

General_screening_panel_v1.4 Summary: Ag3476 Highest expression of the CG59572-01 gene is detected in a breast cancer cell line sample (CT=27.4). Furthermore, moderate to high expression of this gene is detected in CNS cancer, colon cancer, gastric cancer, pancreatic

cancer, lung cancer, ovarian cancer, and prostate cancer. Therefore, therapeutic modulation of the activity of this gene or its protein product, through the use of small molecule drugs, protein therapeutics or antibodies, might be beneficial in the treatment of these cancers.

This gene is expressed at low to moderate levels throughout the CNS, including in amygdala, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord. Therefore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

Among tissues with metabolic function, this gene is expressed at moderate to low levels in pituitary, adipose, adrenal gland, pancreas, thyroid, and adult and fetal skeletal muscle, heart, and liver. This widespread expression among these tissues suggests that this gene product may play a role in normal neuroendocrine and metabolic and that dysregulated expression of this gene may contribute to neuroendocrine disorders or metabolic diseases, such as obesity and diabetes.

In addition, this gene is expressed at much higher levels in fetal lung and liver tissue (CTs=30) when compared to expression in the adult counterpart (CTs=33). Thus, expression of this gene may be used to differentiate between the fetal and adult source of these tissues.

Panel 4D Summary: Ag3476 Highest expression of the CG59572-01 gene is detected in TNFalpha + IL-1beta treated keratinocytes (CT=27.2). Expression of this gene appears to be stimulated in activated secondary Th1, Th2 and Tr1 cells, PWM treated PBMCs, PWM treated B-lymphocytes, IL-2/IL-2+IL-12/IL-2+IFN gamma/IL-2+IL-18 treated LAK cells, and TNFalpha + IL-1beta treated small airway epithelium (CTs=28-30). Thus, this gene may be important in the activation of T and B cells or the function of activated T and B cells. Therefore, small molecules that antagonize the function of this gene product may reduce or eliminate the symptoms in patients with autoimmune and inflammatory diseases in which B and T cells play a part in the initiation or progression of the disease process, such as systemic lupus erythematosus, Crohn's disease, ulcerative colitis, multiple sclerosis, chronic obstructive pulmonary disease, asthma, emphysema, rheumatoid arthritis, or psoriasis.

BX. CG59522-01: Myosin I

Expression of gene CG59522-01 was assessed using the primer-probe set Ag3456, described in Table BXA. Results of the RTQ-PCR runs are shown in Table BXB.

Table BXA. Probe Name Ag3456

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-atgaactgcacttggagagaaa-3'	22	664	629
Probe	TET-5'-aatttcacacaccaggagcaggact-3'- TAMRA	26	699	630
Reverse	5'-ctctgctcatcactcacagtca-3'	22	730	631

Table BXB. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3456, Run 166397214	Tissue Name	Rel. Exp.(%) Ag3456, Run 166397214
Secondary Th1 act	20.2	HUVEC IL-1beta	0.0
Secondary Th2 act	19.6	HUVEC IFN gamma	0.0
Secondary Tr1 act	35.4	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	34.2	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	17.3	HUVEC IL-11	0.0
Secondary Tr1 rest	20.7	Lung Microvascular EC none	0.0
Primary Th1 act	10.6	Lung Microvascular EC TNFalpha + IL-1beta	0.0
Primary Th2 act	13.3	Microvascular Dermal EC none	0.0
Primary Tr1 act	25.2	Microvascular Dermal EC TNFalpha + IL-1beta	0.0
Primary Th1 rest	100.0	Bronchial epithelium TNFalpha + IL1beta	0.0
Primary Th2 rest	35.1	Small airway epithelium none	0.0
Primary Tr1 rest	25.9	Small airway epithelium TNFalpha + IL-1beta	0.0
CD45RA CD4 lymphocyte act	9.9	Coronary artery SMC rest	0.0
CD45RO CD4 lymphocyte act	28.9	Coronary artery SMC TNFalpha + IL-1beta	0.0
CD8 lymphocyte act	27.5	Astrocytes rest	0.0
Secondary CD8 lymphocyte rest	15.6	Astrocytes TNFalpha + IL-1beta	0.0
Secondary CD8 lymphocyte act	26.6	KU-812 (Basophil) rest	2.2
CD4 lymphocyte none	5.0	KU-812 (Basophil) PMA/ionomycin	5.2

2ry Th1/Th2/Tr1_anti- CD95 CH11	31.2	CCD1106 (Keratinocytes) none	0.0
LAK cells rest	4.7	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	1.0
LAK cells IL-2	41.5	Liver cirrhosis	0.8
LAK cells IL-2+IL-12	22.4	Lupus kidney	0.4
LAK cells IL-2+IFN gamma	29.5	NCI-H292 none	0.3
LAK cells IL-2+ IL-18	25.7	NCI-H292 IL-4	0.1
LAK cells PMA/ionomycin	4.4	NCI-H292 IL-9	0.0
NK Cells IL-2 rest	22.2	NCI-H292 IL-13	0.0
Two Way MLR 3 day	14.2	NCI-H292 IFN gamma	0.0
Two Way MLR 5 day	16.0	HPAEC none	0.0
Two Way MLR 7 day	17.2	HPAEC TNF alpha + IL-1 beta	0.0
PBMC rest	7.5	Lung fibroblast none	0.0
PBMC PWM	33.9	Lung fibroblast TNF alpha + IL-1 beta	0.0
PBMC PHA-L	12.7	Lung fibroblast IL-4	0.0
Ramos (B cell) none	4.7	Lung fibroblast IL-9	0.0
Ramos (B cell) ionomycin	8.5	Lung fibroblast IL-13	0.1
B lymphocytes PWM	25.5	Lung fibroblast IFN gamma	0.0
B lymphocytes CD40L and IL-4	18.8	Dermal fibroblast CCD1070 rest	0.0
EOL-1 dbcAMP	17.3	Dermal fibroblast CCD1070 TNF alpha	43.5
EOL-1 dbcAMP PMA/ionomycin	9.9	Dermal fibroblast CCD1070 IL-1 beta	0.0
Dendritic cells none	2.1	Dermal fibroblast IFN gamma	0.0
Dendritic cells LPS	16.4	Dermal fibroblast IL-4	0.0
Dendritic cells anti- CD40	1.6	IBD Colitis 2	0.3
Monocytes rest	20.9	IBD Crohn's	0.1
Monocytes LPS	45.7	Colon	4.2
Macrophages rest	1.3	Lung	2.5
Macrophages LPS	16.3	Thymus	0.0
HUVEC none	0.0	Kidney	11.3
HUVEC starved	0.0		

CNS_neurodegeneration_v1.0 Summary: Ag3456 Expression of CG59522-01 gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.4 Summary: Ag3456 Expression of CG59522-01 gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Panel 4D Summary: Ag3456 Highest expression of the CG59522-01 gene is detected in sample derived from resting primary Th1 cells (CT=29.8). Thus, expression of this gene can be used to distinguish this sample from other samples in this panel. This gene is also expressed at low but significant levels in T cells prepared under a number of conditions, LAK cells, macrophages and dendritic cells also express the transcript. The only non-hematopoietic cell type that expresses the transcript detected by this primer and probe at significant levels is dermal fibroblasts. Colon and kidney also express low levels of the transcript. Thus, this transcript or the protein it encodes could be used to detect hematopoietically-derived cells. Furthermore, therapeutics designed with the protein encoded by this transcript could be important in the regulation the function of antigen presenting cells (macrophages and dendritic cells) or T cells and be important in the treatment of asthma, emphysema, psoriasis, arthritis, and IBD. Therefore, therapeutics designed with the protein encoded for by this transcript could be important in regulating T cell function and treating T and B cell mediated diseases such as asthma, arthritis, psoriasis, IBD, and systemic lupus erythematosus.

BY. CG59520-01: FARNESYL PYROPHOSPHATE SYNTHETASE

Expression of gene CG59520-01 was assessed using the primer-probe set Ag5923, described in Table BYA. Results of the RTQ-PCR runs are shown in Tables BYB and BYC.

Table BYA. Probe Name Ag5923

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-gaatgggaaccagaaatcag-3'	21	5	632
Probe	TET-5'-tttatgcccaagcaaagcaggatttc-3'- TAMRA	26	29	633
Reverse	5'-accctaacgatctgggagtagt-3'	22	62	634

Table BYB. General_screening_panel_v1.5

Tissue Name	Rel. Exp.(%) Ag5923, Run 247608956	Tissue Name	Rel. Exp.(%) Ag5923, Run 247608956
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Adipose	0.6	Renal ca. TK-10	12.1
Melanoma* Hs688(A).T	1.9	Bladder	7.1
Melanoma* Hs688(B).T	2.9	Gastric ca. (liver met.) NCI-N87	26.2
Melanoma* M14	8.9	Gastric ca. KATO III	31.0
Melanoma* LOXIMVI	3.9	Colon ca. SW-948	6.8
Melanoma* SK- MEL-5	2.4	Colon ca. SW480	15.3
Squamous cell carcinoma SCC-4	1.8	Colon ca.* (SW480 met) SW620	8.2
Testis Pool	15.1	Colon ca. HT29	1.9
Prostate ca.* (bone met) PC-3	5.6	Colon ca. HCT-116	9.3
Prostate Pool	2.3	Colon ca. CaCo-2	6.4
Placenta	2.3	Colon cancer tissue	7.3
Uterus Pool	0.0	Colon ca. SW1116	7.1
Ovarian ca. OVCAR-3	6.7	Colon ca. Colo-205	9.5
Ovarian ca. SK-OV- 3	14.8	Colon ca. SW-48	3.8
Ovarian ca. OVCAR-4	4.2	Colon Pool	5.6
Ovarian ca. OVCAR-5	23.0	Small Intestine Pool	7.0
Ovarian ca. IGROV- 1	4.1	Stomach Pool	0.6
Ovarian ca. OVCAR-8	0.7	Bone Marrow Pool	2.1
Ovary	12.1	Fetal Heart	4.1
Breast ca. MCF-7	4.4	Heart Pool	1.1
Breast ca. MDA- MB-231	6.8	Lymph Node Pool	7.3
Breast ca. BT 549	17.8	Fetal Skeletal Muscle	1.0
Breast ca. T47D	5.6	Skeletal Muscle Pool	5.3
Breast ca. MDA-N	2.5	Spleen Pool	2.0
Breast Pool	9.5	Thymus Pool	8.0
Trachea	14.1	CNS cancer (glio/astro) U87-MG	1.7
Lung	13.9	CNS cancer (glio/astro) U-118-MG	10.2
Fetal Lung	16.7	CNS cancer (neuro;met) SK-N-AS	2.8

Lung ca. NCI-N417	1.7	CNS cancer (astro) SF-539	2.8
Lung ca. LX-1	12.8	CNS cancer (astro) SNB-75	14.2
Lung ca. NCI-H146	1.6	CNS cancer (glio) SNB-19	3.9
Lung ca. SHP-77	1.5	CNS cancer (glio) SF-295	10.8
Lung ca. A549	11.0	Brain (Amygdala) Pool	1.8
Lung ca. NCI-H526	0.5	Brain (cerebellum)	4.0
Lung ca. NCI-H23	10.9	Brain (fetal)	4.6
Lung ca. NCI-H460	4.1	Brain (Hippocampus) Pool	3.3
Lung ca. HOP-62	2.3	Cerebral Cortex Pool	0.0
Lung ca. NCI-H522	5.2	Brain (Substantia nigra) Pool	3.2
Liver	0.5	Brain (Thalamus) Pool	1.6
Fetal Liver	4.3	Brain (whole)	1.8
Liver ca. HepG2	0.3	Spinal Cord Pool	1.7
Kidney Pool	13.6	Adrenal Gland	1.7
Fetal Kidney	7.1	Pituitary gland Pool	0.0
Renal ca. 786-0	11.7	Salivary Gland	1.2
Renal ca. A498	5.6	Thyroid (female)	0.5
Renal ca. ACHN	6.2	Pancreatic ca. CAPAN2	100.0
Renal ca. UO-31	14.0	Pancreas Pool	15.3

Table BYC. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag5923, Run 247579946	Tissue Name	Rel. Exp.(%) Ag5923, Run 247579946
Secondary Th1 act	14.6	HUVEC IL-1beta	5.3
Secondary Th2 act	36.6	HUVEC IFN gamma	12.1
Secondary Tr1 act	5.6	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	10.5	HUVEC IL-11	6.7
Secondary Tr1 rest	0.0	Lung Microvascular EC none	15.5
Primary Th1 act	0.0	Lung Microvascular EC TNFalpha + IL-1beta	2.4
Primary Th2 act	11.1	Microvascular Dermal EC none	0.0
Primary Tr1 act	11.0	Microvascular Dermal EC	5.0

		TNFalpha + IL-1beta	
Primary Th1 rest	0.0	Bronchial epithelium TNFalpha + IL1beta	13.5
Primary Th2 rest	1.5	Small airway epithelium none	7.2
Primary Tr1 rest	1.3	Small airway epithelium TNFalpha + IL-1beta	44.8
CD45RA CD4 lymphocyte act	13.5	Coronary artery SMC rest	1.6
CD45RO CD4 lymphocyte act	12.9	Coronary artery SMC TNFalpha + IL-1beta	6.7
CD8 lymphocyte act	1.8	Astrocytes rest	1.5
Secondary CD8 lymphocyte rest	3.6	Astrocytes TNFalpha + IL-1beta	0.0
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	15.3
2ry Th1/Th2/Tr1_anti- CD95 CH11	0.0	CCD1106 (Keratinocytes) none	21.5
LAK cells rest	15.9	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	31.9
LAK cells IL-2	3.5	Liver cirrhosis	4.0
LAK cells IL-2+IL-12	0.0	NCI-H292 none	61.1
LAK cells IL-2+IFN gamma	2.3	NCI-H292 IL-4	100.0
LAK cells IL-2+ IL-18	0.0	NCI-H292 IL-9	45.1
LAK cells PMA/ionomycin	13.0	NCI-H292 IL-13	47.0
NK Cells IL-2 rest	37.1	NCI-H292 IFN gamma	14.5
Two Way MLR 3 day	4.9	HPAEC none	0.0
Two Way MLR 5 day	0.0	HPAEC TNF alpha + IL-1 beta	24.1
Two Way MLR 7 day	1.2	Lung fibroblast none	6.0
PBMC rest	0.0	Lung fibroblast TNF alpha + IL-1 beta	3.7
PBMC PWM	0.0	Lung fibroblast IL-4	1.0
PBMC PHA-L	0.0	Lung fibroblast IL-9	8.7
Ramos (B cell) none	0.0	Lung fibroblast IL-13	0.0
Ramos (B cell) ionomycin	17.7	Lung fibroblast IFN gamma	3.8
B lymphocytes PWM	11.4	Dermal fibroblast CCD1070 rest	5.8
B lymphocytes CD40L and IL-4	23.2	Dermal fibroblast CCD1070 TNF alpha	21.3

EOL-1 dbcAMP	21.0	Dermal fibroblast CCD1070 IL-1 beta	8.6
EOL-1 dbcAMP PMA/ionomycin	3.5	Dermal fibroblast IFN gamma	12.9
Dendritic cells none	11.7	Dermal fibroblast IL-4	13.8
Dendritic cells LPS	8.4	Dermal Fibroblasts rest	0.0
Dendritic cells anti- CD40	3.8	Neutrophils TNFa+LPS	1.5
Monocytes rest	0.0	Neutrophils rest	18.0
Monocytes LPS	57.8	Colon	0.0
Macrophages rest	1.7	Lung	0.0
Macrophages LPS	9.8	Thymus	8.8
HUVEC none	3.1	Kidney	4.0
HUVEC starved	2.5		

CNS_neurodegeneration_v1.0 Summary: Ag5923 Expression of the CG59520-01 gene is low/undetectable (CTs > 34.5) across all of the samples on this panel (data not shown).

General_screening_panel_v1.5 Summary: Ag5923 Highest expression of the CG59520-01 gene is detected in sample derived from a pancreatic cancer cell line (CT=31.5). Thus, expression of this gene can be used in distinguishing this sample from other samples from the panel and as a marker for pancreatic cancer. In addition low levels of expression of this gene are associated with samples derived from CNS, colon, gastric, renal, lung, breast, ovarian and melanoma cancer cell lines. This gene encodes a farnesyl pyrophosphate synthetase, which is involved in cholesterol biosynthesis. It has been suggested that in several types of cancer, activation of p21 would be aided by continuous farnesylation due to stimulation of the cholesterol biosynthetic pathway in tumors (Rao, 1995). Therefore, therapeutic modulation of the activity of protein encoded by this gene may be beneficial in the treatment of these cancers.

In addition, low but significant levels of expression in the pancreas suggest that this gene product may be useful in the treatment of type II diabetes.

References:

1. Rao KN. (1995) The significance of the cholesterol biosynthetic pathway in cell growth and carcinogenesis (review). *Anticancer Res* 1995 Mar-Apr;15(2):309-14

Panel 4.1D Summary: Ag5923 High expression of the CG59520-01 gene is detected in sample derived from untreated and IL4 treated NCI-H292 cells (CTs=33). Thus, expression of this gene could be used to distinguish these samples from other samples from the panel. Also, therapeutic modulation of the activity of this gene product may be beneficial in the treatment asthma and emphysema.

Panel 5 Islet Summary: Ag5923 Expression of the CG59520-01 gene is low/undetectable (CTs > 34.5) across all of the samples on this panel (data not shown).

BZ. CG59704-01: Serine/Threonine Kinase

Expression of gene CG59704-01 was assessed using the primer-probe set Ag3509, described in Table BZA. Results of the RTQ-PCR runs are shown in Tables BZB, BZC and BZD.

Table BZA. Probe Name Ag3509

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5' -gacttcctcacctagcttctg-3'	22	4228	635
Probe	TET-5' -actgcatgccaccactgctgagta-3' - TAMRA	24	4257	636
Reverse	5' -caccaacctagcaaacaacag-3'	22	4281	637

Table BZB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3509, Run 210499481	Tissue Name	Rel. Exp.(%) Ag3509, Run 210499481
AD 1 Hippo	20.2	Control (Path) 3 Temporal Ctx	24.1
AD 2 Hippo	20.2	Control (Path) 4 Temporal Ctx	20.7
AD 3 Hippo	23.3	AD 1 Occipital Ctx	16.4
AD 4 Hippo	13.5	AD 2 Occipital Ctx (Missing)	0.0
AD 5 Hippo	66.4	AD 3 Occipital Ctx	9.9
AD 6 Hippo	84.7	AD 4 Occipital Ctx	4.6
Control 2 Hippo	18.0	AD 5 Occipital Ctx	30.4
Control 4 Hippo	0.4	AD 6 Occipital Ctx	0.0
Control (Path) 3 Hippo	0.3	Control 1 Occipital Ctx	10.0
AD 1 Temporal Ctx	23.7	Control 2 Occipital	35.6

		Ctx	
AD 2 Temporal Ctx	15.4	Control 3 Occipital Ctx	16.3
AD 3 Temporal Ctx	10.8	Control 4 Occipital Ctx	25.2
AD 4 Temporal Ctx	18.8	Control (Path) 1 Occipital Ctx	57.4
AD 5 Inf Temporal Ctx	100.0	Control (Path) 2 Occipital Ctx	8.1
AD 5 Sup Temporal Ctx	72.2	Control (Path) 3 Occipital Ctx	5.4
AD 6 Inf Temporal Ctx	21.9	Control (Path) 4 Occipital Ctx	30.4
AD 6 Sup Temporal Ctx	62.4	Control 1 Parietal Ctx	12.1
Control 1 Temporal Ctx	5.4	Control 2 Parietal Ctx	54.0
Control 2 Temporal Ctx	30.6	Control 3 Parietal Ctx	12.0
Control 3 Temporal Ctx	6.0	Control (Path) 1 Parietal Ctx	51.4
Control 3 Temporal Ctx	12.2	Control (Path) 2 Parietal Ctx	16.0
Control (Path) 1 Temporal Ctx	40.9	Control (Path) 3 Parietal Ctx	2.1
Control (Path) 2 Temporal Ctx	31.9	Control (Path) 4 Parietal Ctx	29.7

Table BZC. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3509, Run 217240617	Tissue Name	Rel. Exp.(%) Ag3509, Run 217240617
Adipose	9.5	Renal ca. TK-10	20.4
Melanoma* Hs688(A).T	8.7	Bladder	16.6
Melanoma* Hs688(B).T	4.5	Gastric ca. (liver met.) NCI-N87	37.6
Melanoma* M14	12.0	Gastric ca. KATO III	23.3
Melanoma* LOXIMVI	3.1	Colon ca. SW-948	6.9
Melanoma* SK- MEL-5	11.0	Colon ca. SW480	35.8
Squamous cell carcinoma SCC-4	9.5	Colon ca.* (SW480 met) SW620	24.7
Testis Pool	5.4	Colon ca. HT29	9.3

Prostate ca.* (bone met) PC-3	24.1	Colon ca. HCT-116	62.4
Prostate Pool	4.5	Colon ca. CaCo-2	8.8
Placenta	1.9	Colon cancer tissue	10.9
Uterus Pool	1.8	Colon ca. SW1116	3.7
Ovarian ca. OVCAR-3	43.2	Colon ca. Colo-205	1.2
Ovarian ca. SK-OV-3	42.3	Colon ca. SW-48	2.8
Ovarian ca. OVCAR-4	1.1	Colon Pool	9.2
Ovarian ca. OVCAR-5	19.1	Small Intestine Pool	8.2
Ovarian ca. IGROV-1	8.7	Stomach Pool	3.7
Ovarian ca. OVCAR-8	7.5	Bone Marrow Pool	4.6
Ovary	3.4	Fetal Heart	7.3
Breast ca. MCF-7	20.7	Heart Pool	5.6
Breast ca. MDA-MB-231	32.8	Lymph Node Pool	10.1
Breast ca. BT 549	35.1	Fetal Skeletal Muscle	6.7
Breast ca. T47D	34.4	Skeletal Muscle Pool	3.6
Breast ca. MDA-N	18.6	Spleen Pool	7.7
Breast Pool	15.7	Thymus Pool	11.0
Trachea	6.8	CNS cancer (glio/astro) U87-MG	27.4
Lung	15.3	CNS cancer (glio/astro) U-118-MG	45.4
Fetal Lung	17.6	CNS cancer (neuro;met) SK-N-AS	16.3
Lung ca. NCI-N417	11.8	CNS cancer (astro) SF-539	9.9
Lung ca. LX-1	29.5	CNS cancer (astro) SNB-75	50.7
Lung ca. NCI-H146	5.6	CNS cancer (glio) SNB-19	7.0
Lung ca. SHP-77	19.1	CNS cancer (glio) SF-295	25.7
Lung ca. A549	17.2	Brain (Amygdala) Pool	4.9
Lung ca. NCI-H526	4.2	Brain (cerebellum)	13.7
Lung ca. NCI-H23	100.0	Brain (fetal)	14.8
Lung ca. NCI-H460	27.2	Brain (Hippocampus) Pool	3.7

Lung ca. HOP-62	16.2	Cerebral Cortex Pool	3.0
Lung ca. NCI-H522	29.9	Brain (Substantia nigra) Pool	1.7
Liver	0.0	Brain (Thalamus) Pool	5.6
Fetal Liver	10.1	Brain (whole)	6.1
Liver ca. HepG2	17.7	Spinal Cord Pool	2.0
Kidney Pool	26.1	Adrenal Gland	8.8
Fetal Kidney	24.3	Pituitary gland Pool	3.4
Renal ca. 786-0	19.8	Salivary Gland	4.9
Renal ca. A498	2.4	Thyroid (female)	3.4
Renal ca. ACHN	8.2	Pancreatic ca. CAPAN2	34.2
Renal ca. UO-31	9.5	Pancreas Pool	16.7

Table BZD. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3509, Run 166407201	Tissue Name	Rel. Exp.(%) Ag3509, Run 166407201
Secondary Th1 act	50.0	HUVEC IL-1beta	4.7
Secondary Th2 act	45.4	HUVEC IFN gamma	4.8
Secondary Tr1 act	87.7	HUVEC TNF alpha + IFN gamma	10.0
Secondary Th1 rest	17.4	HUVEC TNF alpha + IL4	19.9
Secondary Th2 rest	21.9	HUVEC IL-11	13.4
Secondary Tr1 rest	32.5	Lung Microvascular EC none	14.1
Primary Th1 act	40.9	Lung Microvascular EC TNFalpha + IL-1beta	24.8
Primary Th2 act	83.5	Microvascular Dermal EC none	22.1
Primary Tr1 act	100.0	Microvascular Dermal EC TNFalpha + IL-1beta	12.2
Primary Th1 rest	75.8	Bronchial epithelium TNFalpha + IL1beta	9.9
Primary Th2 rest	31.0	Small airway epithelium none	7.7
Primary Tr1 rest	41.5	Small airway epithelium TNFalpha + IL-1beta	23.0
CD45RA CD4 lymphocyte act	21.9	Coronary artery SMC rest	7.6
CD45RO CD4 lymphocyte act	56.6	Coronary artery SMC TNFalpha + IL-1beta	2.0
CD8 lymphocyte act	58.6	Astrocytes rest	25.5
Secondary CD8	51.4	Astrocytes TNFalpha +	28.5

lymphocyte rest		IL-1beta	
Secondary CD8 lymphocyte act	52.1	KU-812 (Basophil) rest	25.5
CD4 lymphocyte none	21.0	KU-812 (Basophil) PMA/ionomycin	68.8
2ry Th1/Th2/Tr1 _anti-CD95 CH11	41.8	CCD1106 (Keratinocytes) none	17.4
LAK cells rest	27.9	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	36.6
LAK cells IL-2	58.6	Liver cirrhosis	57.8
LAK cells IL-2+IL-12	61.1	Lupus kidney	24.3
LAK cells IL-2+IFN gamma	85.3	NCI-H292 none	20.0
LAK cells IL-2+ IL-18	61.1	NCI-H292 IL-4	21.6
LAK cells PMA/ionomycin	49.3	NCI-H292 IL-9	24.5
NK Cells IL-2 rest	43.2	NCI-H292 IL-13	24.8
Two Way MLR 3 day	50.0	NCI-H292 IFN gamma	14.8
Two Way MLR 5 day	39.5	HPAEC none	9.5
Two Way MLR 7 day	37.1	HPAEC TNF alpha + IL-1 beta	25.9
PBMC rest	15.1	Lung fibroblast none	19.6
PBMC PWM	44.8	Lung fibroblast TNF alpha + IL-1 beta	21.3
PBMC PHA-L	14.8	Lung fibroblast IL-4	18.8
Ramos (B cell) none	75.3	Lung fibroblast IL-9	17.8
Ramos (B cell) ionomycin	17.8	Lung fibroblast IL-13	21.9
B lymphocytes PWM	33.4	Lung fibroblast IFN gamma	21.3
B lymphocytes CD40L and IL-4	42.3	Dermal fibroblast CCD1070 rest	46.7
EOL-1 dbcAMP	25.3	Dermal fibroblast CCD1070 TNF alpha	69.3
EOL-1 dbcAMP PMA/ionomycin	18.9	Dermal fibroblast CCD1070 IL-1 beta	20.3
Dendritic cells none	10.7	Dermal fibroblast IFN gamma	17.4
Dendritic cells LPS	13.6	Dermal fibroblast IL-4	21.8
Dendritic cells anti-CD40	12.2	IBD Colitis 2	7.1
Monocytes rest	10.0	IBD Crohn's	5.5
Monocytes LPS	25.3	Colon	53.6
Macrophages rest	29.3	Lung	5.6

Macrophages LPS	7.2	Thymus	27.5
HUVEC none	24.1	Kidney	51.4
HUVEC starved	33.9		

CNS_neurodegeneration_v1.0 Summary: Ag3509 This panel confirms the expression of this gene at low levels in the brain in an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment.

General_screening_panel_v1.4 Summary: Ag3509 Highest expression of the CG59704-01 gene is detected in a sample derived from a lung cancer cell line (CT=31.69). Thus, expression of this gene can be used in distinguishing this sample from other samples in this panel. Furthermore, moderate expression of this gene is associated with cell lines derived from pancreatic, brain, colon, gastric, renal, lung, breast and ovarian cancers. Therefore, therapeutic modulation of the activity of this gene or its protein product, through the use of small molecule drugs, or antibodies, might be beneficial in the treatment of these cancers.

Panel 4D Summary: Ag3509 Expression of the CG59704-01 gene is stimulated in T cells, LAK cells and B cells, with highest expression in primary activated Tr1 cells (CT=32). Therefore, therapeutics designed with the protein encoded for by this transcript could be important in regulating T and B cell function and treating T cell/B cell mediated diseases such as asthma, arthritis, psoriasis, IBD, allergies, hypersensitivity reactions, microbial and viral infections systemic lupus erythematosus, multiple sclerosis, chronic obstructive pulmonary disease and systemic lupus erythematosus.

Furthermore, expression of this gene is decreased in colon samples from patients with IBD colitis and Crohn's disease relative to normal colon. Therefore, therapeutic modulation of the activity of this gene product may be useful in the treatment of inflammatory bowel disease.

Panel 5 Islet Summary: Ag3509 Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

CA. CG59628-01: short-chain dehydrogenase like homo sapiens

Expression of gene CG59628-01 was assessed using the primer-probe set Ag3500, described in Table CAA. Results of the RTQ-PCR runs are shown in Tables CAB and CAC.

Table CAA. Probe Name Ag3500

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-gcagatgtggtgatgagtatga-3'	22	1159	638
Probe	TET-5'-tcaggtaaactaaaaccaacaatggca-3'- TAMRA	27	1207	639
Reverse	5'-atcttcaatttcctgacatga-3'	22	1235	640

Table CAB. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3500, Run 217131378	Tissue Name	Rel. Exp.(%) Ag3500, Run 217131378
Adipose	25.0	Renal ca. TK-10	82.4
Melanoma* Hs688(A).T	19.3	Bladder	15.6
Melanoma* Hs688(B).T	18.3	Gastric ca. (liver met.) NCI-N87	36.3
Melanoma* M14	33.9	Gastric ca. KATO III	51.1
Melanoma* LOXIMVI	36.3	Colon ca. SW-948	17.8
Melanoma* SK- MEL-5	61.1	Colon ca. SW480	66.4
Squamous cell carcinoma SCC-4	17.0	Colon ca.* (SW480 met) SW620	36.1
Testis Pool	11.4	Colon ca. HT29	31.6
Prostate ca.* (bone met) PC-3	35.1	Colon ca. HCT-116	46.0
Prostate Pool	3.9	Colon ca. CaCo-2	58.6
Placenta	1.2	Colon cancer tissue	24.1
Uterus Pool	1.9	Colon ca. SW1116	6.7
Ovarian ca. OVCAR-3	12.2	Colon ca. Colo-205	12.1
Ovarian ca. SK-OV- 3	55.9	Colon ca. SW-48	25.0
Ovarian ca. OVCAR-4	7.2	Colon Pool	16.2
Ovarian ca. OVCAR-5	47.6	Small Intestine Pool	9.9
Ovarian ca. IGROV- 1	23.8	Stomach Pool	6.2
Ovarian ca. OVCAR-8	16.5	Bone Marrow Pool	4.6
Ovary	31.2	Fetal Heart	27.0

Breast ca. MCF-7	9.7	Heart Pool	12.9
Breast ca. MDA-MB-231	33.2	Lymph Node Pool	13.1
Breast ca. BT 549	42.0	Fetal Skeletal Muscle	13.7
Breast ca. T47D	90.8	Skeletal Muscle Pool	40.9
Breast ca. MDA-N	18.9	Spleen Pool	11.6
Breast Pool	14.1	Thymus Pool	13.4
Trachea	7.7	CNS cancer (glio/astro) U87-MG	27.0
Lung	8.1	CNS cancer (glio/astro) U-118-MG	39.0
Fetal Lung	27.7	CNS cancer (neuro;met) SK-N-AS	20.0
Lung ca. NCI-N417	4.4	CNS cancer (astro) SF-539	15.0
Lung ca. LX-1	30.1	CNS cancer (astro) SNB-75	100.0
Lung ca. NCI-H146	1.7	CNS cancer (glio) SNB-19	22.5
Lung ca. SHP-77	27.4	CNS cancer (glio) SF-295	20.6
Lung ca. A549	24.5	Brain (Amygdala) Pool	4.5
Lung ca. NCI-H526	5.6	Brain (cerebellum)	1.8
Lung ca. NCI-H23	23.8	Brain (fetal)	2.0
Lung ca. NCI-H460	22.2	Brain (Hippocampus) Pool	9.2
Lung ca. HOP-62	14.4	Cerebral Cortex Pool	11.7
Lung ca. NCI-H522	24.0	Brain (Substantia nigra) Pool	7.7
Liver	1.2	Brain (Thalamus) Pool	10.1
Fetal Liver	28.7	Brain (whole)	2.8
Liver ca. HepG2	36.6	Spinal Cord Pool	17.2
Kidney Pool	10.8	Adrenal Gland	18.6
Fetal Kidney	13.6	Pituitary gland Pool	2.4
Renal ca. 786-0	44.1	Salivary Gland	1.7
Renal ca. A498	13.7	Thyroid (female)	11.3
Renal ca. ACHN	19.1	Pancreatic ca. CAPAN2	34.9
Renal ca. UO-31	37.4	Pancreas Pool	22.8

Table CAC. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3500, Run 166441942	Tissue Name	Rel. Exp.(%) Ag3500, Run 166441942
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Secondary Th1 act	6.0	HUVEC IL-1beta	6.8
Secondary Th2 act	10.1	HUVEC IFN gamma	17.1
Secondary Tr1 act	14.0	HUVEC TNF alpha + IFN gamma	5.6
Secondary Th1 rest	4.1	HUVEC TNF alpha + IL4	6.2
Secondary Th2 rest	2.4	HUVEC IL-11	7.2
Secondary Tr1 rest	3.1	Lung Microvascular EC none	6.0
Primary Th1 act	1.7	Lung Microvascular EC TNFalpha + IL-1beta	4.5
Primary Th2 act	6.4	Microvascular Dermal EC none	20.0
Primary Tr1 act	10.5	Microvascular Dermal EC TNFalpha + IL-1beta	5.9
Primary Th1 rest	20.3	Bronchial epithelium TNFalpha + IL1beta	6.8
Primary Th2 rest	9.8	Small airway epithelium none	11.2
Primary Tr1 rest	18.0	Small airway epithelium TNFalpha + IL-1beta	50.7
CD45RA CD4 lymphocyte act	11.5	Coronary artery SMC rest	6.8
CD45RO CD4 lymphocyte act	8.5	Coronary artery SMC TNFalpha + IL-1beta	5.7
CD8 lymphocyte act	13.2	Astrocytes rest	17.9
Secondary CD8 lymphocyte rest	6.9	Astrocytes TNFalpha + IL-1beta	26.2
Secondary CD8 lymphocyte act	6.2	KU-812 (Basophil) rest	13.2
CD4 lymphocyte none	2.1	KU-812 (Basophil) PMA/ionomycin	23.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	3.2	CCD1106 (Keratinocytes) none	14.5
LAK cells rest	2.5	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	68.8
LAK cells IL-2	12.2	Liver cirrhosis	20.4
LAK cells IL-2+IL-12	9.8	Lupus kidney	13.5
LAK cells IL-2+IFN gamma	11.7	NCI-H292 none	47.0
LAK cells IL-2+ IL-18	8.0	NCI-H292 IL-4	21.8
LAK cells PMA/ionomycin	2.0	NCI-H292 IL-9	29.5
NK Cells IL-2 rest	6.3	NCI-H292 IL-13	13.3
Two Way MLR 3 day	6.4	NCI-H292 IFN gamma	12.3
Two Way MLR 5 day	12.3	HPAEC none	10.5

Two Way MLR 7 day	6.3	HPAEC TNF alpha + IL-1 beta	7.3
PBMC rest	3.3	Lung fibroblast none	10.1
PBMC PWM	11.6	Lung fibroblast TNF alpha + IL-1 beta	15.1
PBMC PHA-L	5.7	Lung fibroblast IL-4	9.1
Ramos (B cell) none	6.1	Lung fibroblast IL-9	9.3
Ramos (B cell) ionomycin	8.3	Lung fibroblast IL-13	8.1
B lymphocytes PWM	27.4	Lung fibroblast IFN gamma	24.5
B lymphocytes CD40L and IL-4	15.0	Dermal fibroblast CCD1070 rest	39.8
EOL-1 dbcAMP	20.7	Dermal fibroblast CCD1070 TNF alpha	47.3
EOL-1 dbcAMP PMA/ionomycin	4.7	Dermal fibroblast CCD1070 IL-1 beta	12.4
Dendritic cells none	6.9	Dermal fibroblast IFN gamma	11.4
Dendritic cells LPS	11.6	Dermal fibroblast IL-4	48.3
Dendritic cells anti-CD40	3.8	IBD Colitis 2	2.2
Monocytes rest	6.0	IBD Crohn's	8.4
Monocytes LPS	2.3	Colon	100.0
Macrophages rest	12.2	Lung	14.0
Macrophages LPS	5.4	Thymus	73.2
HUVEC none	19.2	Kidney	25.0
HUVEC starved	31.9		

CNS_neurodegeneration_v1.0 Summary: Ag3500 Results from one experiment with the CG59628-01 gene are not included. The amp plot indicates that there were experimental difficulties with this run.

General_screening_panel_v1.4 Summary: Ag3500 Highest expression of the CG59628-01 gene is detected in a sample derived from a CNS cancer cell line (CT=31.1). Therefore, expression of this gene may be used to distinguish this sample from the other samples on this panel. In addition, significant expression of this gene is associated with samples derived from colon, ovarian, breast, renal, lung, melanoma, and brain cancer cell lines. Therefore, therapeutic modulation of the activity of this gene or its protein product might be beneficial in the treatment of these cancers.

Among tissues with metabolic function, this gene is expressed at low but significant levels in pituitary, adipose, adrenal gland, pancreas, thyroid, and adult and fetal skeletal muscle, heart, and liver. This widespread expression among these tissues suggests that this gene product may play a role in normal neuroendocrine and metabolic and that dysregulated expression of this gene may contribute to neuroendocrine disorders or metabolic diseases, such as obesity and diabetes.

This molecule is also expressed at low levels in the CNS, including the hippocampus, thalamus, substantia nigra and cerebral cortex. Therefore, therapeutic modulation of the expression or function of this gene may be useful in the treatment of neurologic disorders, such as Alzheimer's disease, Parkinson's disease, schizophrenia, multiple sclerosis, stroke and epilepsy.

Panel 4D Summary: Ag3500 Highest expression of the CG59628-01 gene is detected in colon (CT=30.3). Therefore, expression of this gene may be used to distinguish colon from the other tissues on this panel. Furthermore, expression of this gene is decreased in colon samples from patients with IBD colitis and Crohn's disease relative to normal colon. Therefore, therapeutic modulation of the activity of the GPCR encoded by this gene may be useful in the treatment of inflammatory bowel disease.

CB. CG59671-02: acetyl-coenzyme A synthetase

Expression of gene CG59671-02 was assessed using the primer-probe sets Ag3506 and Ag3581, described in Tables CBA and CBB. Results of the RTQ-PCR runs are shown in Tables CBC, CBD, CBE and CBF.

Table CBA. Probe Name Ag3506

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-aggacacagctacgtggtgtat-3'	22	1072	641
Probe	TET-5'-cctctctgcaatggtgccaccag-3'-TAMRA	23	1097	642
Reverse	5'-gataaactggggtgctctcaa-3'	21	1128	643

Table CBB. Probe Name Ag3581

Primers	Sequences	Length	Start Position	SEQ ID NO:
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Forward	5'-aggacacagctacgtggtgtat-3'	22	1072	644
Probe	TET-5'-cctctctgcaatggtgccaccag-3'-TAMRA	23	1097	645
Reverse	5'-gataaactggggtgctctcaa-3'	21	1128	646

Table CBC. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3506, Run 210497900	Rel. Exp.(%) Ag3581, Run 210643840	Tissue Name	Rel. Exp.(%) Ag3506, Run 210497900	Rel. Exp.(%) Ag3581, Run 210643840
AD 1 Hippo	30.1	36.9	Control (Path) 3 Temporal Ctx	15.8	21.5
AD 2 Hippo	87.7	89.5	Control (Path) 4 Temporal Ctx	42.6	53.6
AD 3 Hippo	12.5	12.5	AD 1 Occipital Ctx	35.6	31.4
AD 4 Hippo	29.1	38.4	AD 2 Occipital Ctx (Missing)	0.0	0.0
AD 5 Hippo	55.5	69.3	AD 3 Occipital Ctx	17.8	18.7
AD 6 Hippo	24.1	33.4	AD 4 Occipital Ctx	47.0	38.4
Control 2 Hippo	42.3	56.3	AD 5 Occipital Ctx	42.9	26.1
Control 4 Hippo	42.6	60.3	AD 6 Occipital Ctx	24.3	51.1
Control (Path) 3 Hippo	19.8	23.0	Control 1 Occipital Ctx	20.3	16.2
AD 1 Temporal Ctx	63.7	48.3	Control 2 Occipital Ctx	71.2	63.7
AD 2 Temporal Ctx	60.7	87.7	Control 3 Occipital Ctx	35.4	41.5
AD 3 Temporal	15.9	15.6	Control 4 Occipital	20.0	27.9

Ctx			Ctx		
AD 4 Temporal Ctx	47.0	57.0	Control (Path) 1 Occipital Ctx	81.2	100.0
AD 5 Inf Temporal Ctx	68.3	72.2	Control (Path) 2 Occipital Ctx	18.9	26.4
AD 5 Sup Temporal Ctx	65.5	57.8	Control (Path) 3 Occipital Ctx	15.7	10.1
AD 6 Inf Temporal Ctx	29.5	35.6	Control (Path) 4 Occipital Ctx	24.8	26.8
AD 6 Sup Temporal Ctx	31.2	31.9	Control 1 Parietal Ctx	21.9	33.7
Control 1 Temporal Ctx	22.5	29.3	Control 2 Parietal Ctx	51.8	79.0
Control 2 Temporal Ctx	55.1	58.6	Control 3 Parietal Ctx	31.4	38.4
Control 3 Temporal Ctx	26.4	34.6	Control (Path) 1 Parietal Ctx	100.0	93.3
Control 3 Temporal Ctx	35.6	35.8	Control (Path) 2 Parietal Ctx	51.1	57.4
Control (Path) 1 Temporal Ctx	62.9	73.7	Control (Path) 3 Parietal Ctx	17.1	17.2
Control (Path) 2 Temporai Ctx	54.0	55.1	Control (Path) 4 Parietal Ctx	54.3	55.9

Table CBD. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3506, Run 217236187	Rel. Exp.(%) Ag3581, Run 217423588	Tissue Name	Rel. Exp.(%) Ag3506, Run 217236187	Rel. Exp.(%) Ag3581, Run 217423588
Adipose	3.6	3.5	Renal ca. TK-10	4.1	3.4

Melanoma* Hs688(A).T	1.8	1.0	Bladder	16.5	12.2
Melanoma* Hs688(B).T	0.6	0.6	Gastric ca. (liver met.) NCI-N87	21.5	17.3
Melanoma* M14	100.0	30.4	Gastric ca. KATO III	63.3	53.2
Melanoma* LOXIMVI	0.0	0.0	Colon ca. SW- 948	8.0	5.0
Melanoma* SK-MEL-5	7.5	100.0	Colon ca. SW480	20.7	16.6
Squamous cell carcinoma SCC-4	10.9	6.3	Colon ca.* (SW480 met) SW620	0.0	0.1
Testis Pool	11.9	9.8	Colon ca. HT29	24.7	15.7
Prostate ca.* (bone met) PC-3	2.0	2.3	Colon ca. HCT- 116	0.0	0.0
Prostate Pool	13.0	7.5	Colon ca. CaCo-2	60.3	40.1
Placenta	87.1	50.3	Colon cancer tissue	30.8	18.8
Uterus Pool	7.0	4.5	Colon ca. SW1116	5.3	2.4
Ovarian ca. OVCAR-3	28.5	14.4	Colon ca. Colo- 205	1.9	1.9
Ovarian ca. SK-OV-3	7.7	4.2	Colon ca. SW-48	33.2	16.8
Ovarian ca. OVCAR-4	2.6	1.0	Colon Pool	14.3	15.1
Ovarian ca. OVCAR-5	28.3	14.1	Small Intestine Pool	15.0	7.4
Ovarian ca. IGROV-1	0.5	0.2	Stomach Pool	8.3	4.8
Ovarian ca. OVCAR-8	1.4	1.1	Bone Marrow Pool	7.3	4.7
Ovary	7.9	7.3	Fetal Heart	16.0	12.8
Breast ca. MCF-7	3.8	2.1	Heart Pool	13.1	10.1
Breast ca. MDA-MB- 231	8.2	6.0	Lymph Node Pool	16.3	9.2
Breast ca. BT 549	1.6	1.2	Fetal Skeletal Muscle	6.9	3.7
Breast ca. T47D	62.9	31.2	Skeletal Muscle Pool	18.9	15.1
Breast ca. MDA-N	29.7	15.4	Spleen Pool	8.8	6.9

Breast Pool	12.5	8.8	Thymus Pool	19.6	11.6
Trachea	12.4	8.2	CNS cancer (glio/astro) U87-MG	0.6	0.3
Lung	1.7	0.8	CNS cancer (glio/astro) U-118-MG	0.4	0.2
Fetal Lung	29.7	18.0	CNS cancer (neuro;met) SK-N-AS	3.4	2.2
Lung ca. NCI-N417	0.1	0.0	CNS cancer (astro) SF-539	0.1	0.0
Lung ca. LX-1	0.1	0.1	CNS cancer (astro) SNB-75	10.4	2.1
Lung ca. NCI-H146	0.3	0.1	CNS cancer (glio) SNB-19	1.0	0.2
Lung ca. SHP-77	7.8	5.0	CNS cancer (glio) SF-295	1.3	0.6
Lung ca. A549	7.8	5.1	Brain (Amygdala) Pool	10.3	5.9
Lung ca. NCI-H526	10.2	2.5	Brain (cerebellum)	32.3	21.0
Lung ca. NCI-H23	3.4	3.2	Brain (fetal)	9.7	4.7
Lung ca. NCI-H460	1.9	0.8	Brain (Hippocampus) Pool	15.5	10.6
Lung ca. HOP-62	0.9	0.6	Cerebral Cortex Pool	20.7	14.5
Lung ca. NCI-H522	0.1	0.1	Brain (Substantia nigra) Pool	18.8	9.9
Liver	0.8	0.5	Brain (Thalamus) Pool	15.9	10.4
Fetal Liver	37.1	22.4	Brain (whole)	20.3	14.3
Liver ca. HepG2	1.8	0.8	Spinal Cord Pool	14.8	9.0
Kidney Pool	18.7	14.9	Adrenal Gland	5.6	3.8
Fetal Kidney	6.2	6.0	Pituitary gland Pool	1.6	1.0
Renal ca. 786-0	0.3	0.1	Salivary Gland	15.3	8.6
Renal ca. A498	1.8	1.1	Thyroid (female)	11.0	11.4
Renal ca. ACHN	4.3	1.4	Pancreatic ca. CAPAN2	0.3	0.2
Renal ca. UO-	9.3	2.5	Pancreas Pool	16.7	16.5

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Table CBE. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag3581, Run 169910402	Tissue Name	Rel. Exp.(%) Ag3581, Run 169910402
Secondary Th1 act	36.6	HUVEC IL-1beta	4.0
Secondary Th2 act	38.2	HUVEC IFN gamma	19.5
Secondary Tr1 act	45.1	HUVEC TNF alpha + IFN gamma	5.3
Secondary Th1 rest	72.2	HUVEC TNF alpha + IL4	2.6
Secondary Th2 rest	58.2	HUVEC IL-11	11.5
Secondary Tr1 rest	79.0	Lung Microvascular EC none	27.9
Primary Th1 act	23.2	Lung Microvascular EC TNFalpha + IL-1beta	28.1
Primary Th2 act	48.6	Microvascular Dermal EC none	7.9
Primary Tr1 act	38.4	Microvascular Dermal EC TNFalpha + IL-1beta	10.6
Primary Th1 rest	90.8	Bronchial epithelium TNFalpha + IL1beta	6.9
Primary Th2 rest	99.3	Small airway epithelium none	1.7
Primary Tr1 rest	90.8	Small airway epithelium TNFalpha + IL-1beta	3.2
CD45RA CD4 lymphocyte act	15.2	Coronary artery SMC rest	0.3
CD45RO CD4 lymphocyte act	45.1	Coronary artery SMC TNFalpha + IL-1beta	0.3
CD8 lymphocyte act	36.3	Astrocytes rest	0.0
Secondary CD8 lymphocyte rest	27.0	Astrocytes TNFalpha + IL-1beta	0.0
Secondary CD8 lymphocyte act	41.2	KU-812 (Basophil) rest	100.0
CD4 lymphocyte none	31.0	KU-812 (Basophil) PMA/ionomycin	25.2
2ry Th1/Th2/Tr1_anti- CD95 CH11	77.4	CCD1106 (Keratinocytes) none	13.0
LAK cells rest	40.6	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	19.3
LAK cells IL-2	66.0	Liver cirrhosis	8.9
LAK cells IL-2+IL-12	28.3	NCI-H292 none	0.5
LAK cells IL-2+IFN	34.9	NCI-H292 IL-4	0.8

gamma			
LAK cells IL-2+ IL-18	32.1	NCI-H292 IL-9	0.8
LAK cells PMA/ionomycin	9.3	NCI-H292 IL-13	1.2
NK Cells IL-2 rest	82.4	NCI-H292 IFN gamma	3.0
Two Way MLR 3 day	59.9	HPAEC none	8.6
Two Way MLR 5 day	28.7	HPAEC TNF alpha + IL-1 beta	7.7
Two Way MLR 7 day	27.4	Lung fibroblast none	1.9
PBMC rest	45.1	Lung fibroblast TNF alpha + IL-1 beta	0.1
PBMC PWM	19.5	Lung fibroblast IL-4	1.2
PBMC PHA-L	28.1	Lung fibroblast IL-9	0.3
Ramos (B cell) none	47.0	Lung fibroblast IL-13	0.6
Ramos (B cell) ionomycin	37.4	Lung fibroblast IFN gamma	2.6
B lymphocytes PWM	16.4	Dermal fibroblast CCD1070 rest	3.6
B lymphocytes CD40L and IL-4	48.6	Dermal fibroblast CCD1070 TNF alpha	73.7
EOL-1 dbcAMP	0.3	Dermal fibroblast CCD1070 IL-1 beta	3.5
EOL-1 dbcAMP PMA/ionomycin	0.0	Dermal fibroblast IFN gamma	8.3
Dendritic cells none	24.0	Dermal fibroblast IL-4	6.1
Dendritic cells LPS	6.5	Dermal Fibroblasts rest	23.0
Dendritic cells anti- CD40	24.1	Neutrophils TNF α +LPS	2.1
Monocytes rest	44.8	Neutrophils rest	8.7
Monocytes LPS	10.7	Colon	69.3
Macrophages rest	38.7	Lung	27.7
Macrophages LPS	9.5	Thymus	75.3
HUVEC none	2.9	Kidney	84.7
HUVEC starved	3.3		

Table CBF. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3506, Run 166407188	Tissue Name	Rel. Exp.(%) Ag3506, Run 166407188
Secondary Th1 act	8.4	HUVEC IL-1beta	0.4
Secondary Th2 act	7.2	HUVEC IFN gamma	6.7
Secondary Tr1 act	11.4	HUVEC TNF alpha + IFN gamma	1.1

Secondary Th1 rest	31.6	HUVEC TNF alpha + IL4	1.0
Secondary Th2 rest	13.7	HUVEC IL-11	2.3
Secondary Tr1 rest	22.5	Lung Microvascular EC none	3.8
Primary Th1 act	3.9	Lung Microvascular EC TNFalpha + IL-1beta	4.0
Primary Th2 act	14.6	Microvascular Dermal EC none	3.4
Primary Tr1 act	14.3	Microvascular Dermal EC TNFalpha + IL-1beta	2.8
Primary Th1 rest	69.7	Bronchial epithelium TNFalpha + IL1beta	0.9
Primary Th2 rest	44.1	Small airway epithelium none	0.2
Primary Tr1 rest	28.9	Small airway epithelium TNFalpha + IL-1beta	1.2
CD45RA CD4 lymphocyte act	3.2	Coronary artery SMC rest	0.0
CD45RO CD4 lymphocyte act	12.3	Coronary artery SMC TNFalpha + IL-1beta	0.3
CD8 lymphocyte act	8.7	Astrocytes rest	0.1
Secondary CD8 lymphocyte rest	9.5	Astrocytes TNFalpha + IL-1beta	0.1
Secondary CD8 lymphocyte act	12.0	KU-812 (Basophil) rest	18.3
CD4 lymphocyte none	9.6	KU-812 (Basophil) PMA/ionomycin	14.9
2ry Th1/Th2/Tr1_anti-CD95 CH11	23.8	CCD1106 (Keratinocytes) none	2.0
LAK cells rest	6.8	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	11.7
LAK cells IL-2	21.2	Liver cirrhosis	5.4
LAK cells IL-2+IL-12	8.5	Lupus kidney	12.2
LAK cells IL-2+IFN gamma	12.2	NCI-H292 none	0.2
LAK cells IL-2+ IL-18	12.0	NCI-H292 IL-4	0.2
LAK cells PMA/ionomycin	1.8	NCI-H292 IL-9	0.2
NK Cells IL-2 rest	16.0	NCI-H292 IL-13	0.0
Two Way MLR 3 day	16.6	NCI-H292 IFN gamma	0.1
Two Way MLR 5 day	7.2	HPAEC none	2.9
Two Way MLR 7 day	9.6	HPAEC TNF alpha + IL-1 beta	2.8
PBMC rest	8.5	Lung fibroblast none	0.5
PBMC PWM	3.5	Lung fibroblast TNF alpha	0.6

		+ IL-1 beta	
PBMC PHA-L	2.8	Lung fibroblast IL-4	0.1
Ramos (B cell) none	11.3	Lung fibroblast IL-9	0.1
Ramos (B cell) ionomycin	5.6	Lung fibroblast IL-13	0.0
B lymphocytes PWM	6.2	Lung fibroblast IFN gamma	0.5
B lymphocytes CD40L and IL-4	12.2	Dermal fibroblast CCD1070 rest	1.1
EOL-1 dbcAMP	0.1	Dermal fibroblast CCD1070 TNF alpha	21.8
EOL-1 dbcAMP PMA/ionomycin	0.0	Dermal fibroblast CCD1070 IL-1 beta	1.0
Dendritic cells none	4.3	Dermal fibroblast IFN gamma	2.1
Dendritic cells LPS	1.4	Dermal fibroblast IL-4	1.8
Dendritic cells anti-CD40	4.6	IBD Colitis 2	2.6
Monocytes rest	11.9	IBD Crohn's	5.5
Monocytes LPS	1.7	Colon	100.0
Macrophages rest	9.3	Lung	5.9
Macrophages LPS	1.6	Thymus	37.9
HUVEC none	0.9	Kidney	24.7
HUVEC starved	1.7		

CNS_neurodegeneration_v1.0 Summary: Ag3506/Ag3581 This panel confirms the expression of the CG59671-02 gene at significant levels in the brain in an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment.

This gene is expressed at moderate levels throughout the CNS, including in amygdala, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord as observed in panel 1.4. Therefore, this gene may play a role in other central nervous system disorders such as, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression

General_screening_panel_v1.4 Summary: Ag3506/Ag3581 Two experiments produce results that are in very good agreement. Highest expression of the CG59671-02 gene is observed in samples derived from melanoma cell lines (CTs=23-35). Thus, expression of this gene can be used in distinguishing these samples from other samples in the panel. In addition,

significant levels of expression of this gene are also associated with colon cancer, ovarian cancer, breast cancer, and lung cancer cell lines. Therefore, therapeutic modulation of the activity of this gene or its protein product might be beneficial in the treatment of these cancers.

This gene is also expressed at low to moderate levels in a number of tissues with metabolic or endocrine function, including adipose, adrenal gland, gastrointestinal tract, pancreas, skeletal muscle and thyroid. Therefore, therapeutic modulation of the activity of this gene may prove useful in the treatment of endocrine/metabolically related diseases, such as obesity and diabetes.

This gene is also expressed at high to moderate levels in all regions of the CNS examined. Please see Panel CNS_neurodegeneration_v1.0 for discussion of utility of this gene in the central nervous system.

Panel 4.1D Summary: Ag3581 Highest expression of the CG59671-02 gene is observed in the resting KU-812 sample (CT=29.18). In addition, high expression of this gene is detected in colon, lung, thymus and kidney. Therefore, therapies designed with the protein encoded for by this gene could be important in the treatment of inflammatory or autoimmune diseases that affect the kidney, lung and kidney including, asthma, allergies, lupus and glomerulonephritis. Expression of this gene is decreased in colon samples from patients with IBD colitis and Crohn's disease relative to normal colon. Therefore, therapeutic modulation of the activity of the protein encoded by this gene may also be useful in the treatment of inflammatory bowel disease.

Expression of this gene appears to be down-regulated in activated primary and secondary Th1, Th2, and Tr1 cells. Also, TNF alpha stimulates the expression of this gene in resting dermal fibroblasts. Therefore, therapeutics designed with the protein encoded by this transcript could be important in regulating T cell function and treating diseases such as asthma, arthritis, psoriasis, IBD, and systemic lupus erythematosus.

Panel 4D Summary: Ag3506 Highest expression of CG59671-02 is observed colon sample (CT=27.3). Overall, the expression pattern using this probe is in excellent agreement with results in panel 4.1D for Ag3581. Please see that panel for discussion of utility of this gene in inflammation.

CC. CG56870-01: NDR3

Expression of gene CG56870-01 was assessed using the primer-probe set Ag2075, described in Table CCA. Results of the RTQ-PCR runs are shown in Tables CCB, CCC, CCD and CCE. Please note that CG56870-02 represents a full-length physical clone of the CG56870-01 gene, validating the prediction of the gene sequence.

Table CCA. Probe Name Ag2075

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-catggatgaacttcaggatgtt-3'	22	70	647
Probe	TET-5'-cagctcacagagatcaaaccacttct-3'- TAMRA	26	92	648
Reverse	5'-tgacagtcaaagtctctggaagt-3'	22	141	649

Table CCB. Panel 1.3D

Tissue Name	Rel. Exp.(%) Ag2075, Run 152355202	Tissue Name	Rel. Exp.(%) Ag2075, Run 152355202
Liver adenocarcinoma	11.9	Kidney (fetal)	1.4
Pancreas	0.8	Renal ca. 786-0	3.5
Pancreatic ca. CAPAN 2	1.6	Renal ca. A498	12.9
Adrenal gland	2.4	Renal ca. RXF 393	1.5
Thyroid	1.8	Renal ca. ACHN	1.7
Salivary gland	1.2	Renal ca. UO-31	6.8
Pituitary gland	2.4	Renal ca. TK-10	2.8
Brain (fetal)	3.2	Liver	0.4
Brain (whole)	25.2	Liver (fetal)	0.8
Brain (amygdala)	14.1	Liver ca. (hepatoblast) HepG2	6.7
Brain (cerebellum)	10.8	Lung	2.1
Brain (hippocampus)	39.8	Lung (fetal)	3.2
Brain (substantia nigra)	2.7	Lung ca. (small cell) LX-1	4.1
Brain (thalamus)	12.4	Lung ca. (small cell) NCI-H69	3.8
Cerebral Cortex	100.0	Lung ca. (s.cell var.) SHP-77	3.8
Spinal cord	3.5	Lung ca. (large cell) NCI-H460	0.6
glio/astro U87-MG	6.4	Lung ca. (non-sm. cell) A549	3.0
glio/astro U-118-MG	10.4	Lung ca. (non-s.cell)	7.7

		NCI-H23	
astrocytoma SW1783	5.1	Lung ca. (non-s.cell) HOP-62	3.1
neuro*; met SK-N-AS	6.2	Lung ca. (non-s.cl) NCI-H522	6.3
astrocytoma SF-539	5.4	Lung ca. (squam.) SW 900	1.4
astrocytoma SNB-75	6.7	Lung ca. (squam.) NCI-H596	1.4
glioma SNB-19	3.1	Mammary gland	2.4
glioma U251	2.0	Breast ca.* (pl.ef) MCF-7	1.8
glioma SF-295	3.4	Breast ca.* (pl.ef) MDA-MB-231	11.6
Heart (fetal)	6.7	Breast ca.* (pl.ef) T47D	9.0
Heart	1.4	Breast ca. BT-549	4.8
Skeletal muscle (fetal)	18.0	Breast ca. MDA-N	4.2
Skeletal muscle	0.7	Ovary	13.4
Bone marrow	0.9	Ovarian ca. OVCAR-3	1.8
Thymus	0.9	Ovarian ca. OVCAR-4	1.6
Spleen	3.7	Ovarian ca. OVCAR-5	1.8
Lymph node	1.9	Ovarian ca. OVCAR-8	4.9
Colorectal	3.3	Ovarian ca. IGROV-1	1.6
Stomach	2.7	Ovarian ca.* (ascites) SK-OV-3	5.8
Small intestine	2.5	Uterus	2.4
Colon ca. SW480	10.4	Placenta	1.2
Colon ca.* SW620(SW480 met)	3.7	Prostate	6.0
Colon ca. HT29	4.6	Prostate ca.* (bone met)PC-3	4.5
Colon ca. HCT-116	3.6	Testis	1.7
Colon ca. CaCo-2	10.3	Melanoma Hs688(A).T	3.8
Colon ca. tissue(ODO3866)	3.2	Melanoma* (met) Hs688(B).T	4.4
Colon ca. HCC-2998	2.6	Melanoma UACC-62	1.4
Gastric ca.* (liver met) NCI-N87	3.1	Melanoma M14	1.8

Bladder	0.8	Melanoma LOX IMVI	3.3
Trachea	2.0	Melanoma* (met) SK-MEL-5	2.4
Kidney	1.3	Adipose	1.2

Table CCC. Panel 2.2

Tissue Name	Rel. Exp.(%) Ag2075, Run 174255357	Tissue Name	Rel. Exp.(%) Ag2075, Run 174255357
Normal Colon	27.7	Kidney Margin (OD04348)	46.3
Colon cancer (OD06064)	52.9	Kidney malignant cancer (OD06204B)	19.2
Colon Margin (OD06064)	30.1	Kidney normal adjacent tissue (OD06204E)	14.3
Colon cancer (OD06159)	5.5	Kidney Cancer (OD04450-01)	66.0
Colon Margin (OD06159)	21.0	Kidney Margin (OD04450-03)	19.8
Colon cancer (OD06297-04)	22.2	Kidney Cancer 8120613	3.0
Colon Margin (OD06297-05)	41.8	Kidney Margin 8120614	11.0
CC Gr.2 ascend colon (ODO3921)	4.0	Kidney Cancer 9010320	6.8
CC Margin (ODO3921)	6.7	Kidney Margin 9010321	9.7
Colon cancer metastasis (OD06104)	11.1	Kidney Cancer 8120607	35.6
Lung Margin (OD06104)	42.6	Kidney Margin 8120608	13.7
Colon mets to lung (OD04451-01)	17.8	Normal Uterus	59.5
Lung Margin (OD04451-02)	9.3	Uterine Cancer 064011	9.7
Normal Prostate	51.4	Normal Thyroid	8.8
Prostate Cancer (OD04410)	23.0	Thyroid Cancer 064010	11.2
Prostate Margin (OD04410)	19.3	Thyroid Cancer A302152	17.9
Normal Ovary	22.8	Thyroid Margin A302153	5.5
Ovarian cancer	9.9	Normal Breast	33.2

(OD06283-03)			
Ovarian Margin (OD06283-07)	17.1	Breast Cancer (OD04566)	8.5
Ovarian Cancer 064008	18.0	Breast Cancer 1024	36.1
Ovarian cancer (OD06145)	6.6	Breast Cancer (OD04590-01)	18.4
Ovarian Margin (OD06145)	12.5	Breast Cancer Mets (OD04590-03)	31.9
Ovarian cancer (OD06455-03)	14.7	Breast Cancer Metastasis (OD04655- 05)	45.4
Ovarian Margin (OD06455-07)	21.8	Breast Cancer 064006	11.5
Normal Lung	21.9	Breast Cancer 9100266	20.9
Invasive poor diff. lung adeno (ODO4945-01)	17.6	Breast Margin 9100265	35.1
Lung Margin (ODO4945-03)	12.2	Breast Cancer A209073	9.7
Lung Malignant Cancer (OD03126)	8.7	Breast Margin A2090734	22.2
Lung Margin (OD03126)	7.4	Breast cancer (OD06083)	100.0
Lung Cancer (OD05014A)	9.9	Breast cancer node metastasis (OD06083)	63.7
Lung Margin (OD05014B)	21.8	Normal Liver	9.9
Lung cancer (OD06081)	5.1	Liver Cancer 1026	5.6
Lung Margin (OD06081)	7.9	Liver Cancer 1025	13.5
Lung Cancer (OD04237-01)	17.4	Liver Cancer 6004-T	4.8
Lung Margin (OD04237-02)	24.0	Liver Tissue 6004-N	9.3
Ocular Melanoma Metastasis	9.7	Liver Cancer 6005-T	15.7
Ocular Melanoma Margin (Liver)	4.6	Liver Tissue 6005-N	20.4
Melanoma Metastasis	19.8	Liver Cancer 064003	10.7
Melanoma Margin (Lung)	21.6	Normal Bladder	8.0
Normal Kidney	11.0	Bladder Cancer 1023	10.5
Kidney Ca, Nuclear grade 2 (OD04338)	37.6	Bladder Cancer A302173	17.3
Kidney Margin (OD04338)	22.1	Normal Stomach	37.9

Kidney Ca Nuclear grade 1/2 (OD04339)	21.6	Gastric Cancer 9060397	11.1
Kidney Margin (OD04339)	12.9	Stomach Margin 9060396	20.6
Kidney Ca, Clear cell type (OD04340)	6.5	Gastric Cancer 9060395	22.7
Kidney Margin (OD04340)	18.4	Stomach Margin 9060394	36.1
Kidney Ca, Nuclear grade 3 (OD04348)	12.9	Gastric Cancer 064005	8.1

Table CCD. Panel 3D

Tissue Name	Rel. Exp.(%) Ag2075, Run 164750734	Tissue Name	Rel. Exp.(%) Ag2075, Run 164750734
Daoy- Medulloblastoma	6.7	Ca Ski- Cervical epidermoid carcinoma (metastasis)	50.3
TE671- Medulloblastoma	9.0	ES-2- Ovarian clear cell carcinoma	13.9
D283 Med- Medulloblastoma	35.4	Ramos- Stimulated with PMA/ionomycin 6h	2.7
PFSK-1- Primitive Neuroectodermal	15.4	Ramos- Stimulated with PMA/ionomycin 14h	3.3
XF-498- CNS	4.4	MEG-01- Chronic myelogenous leukemia (megakaryoblast)	3.4
SNB-78- Glioma	23.3	Raji- Burkitt's lymphoma	3.7
SF-268- Glioblastoma	13.6	Daudi- Burkitt's lymphoma	6.5
T98G- Glioblastoma	18.6	U266- B-cell plasmacytoma	8.4
SK-N-SH- Neuroblastoma (metastasis)	17.0	CA46- Burkitt's lymphoma	7.2
SF-295- Glioblastoma	8.4	RL- non-Hodgkin's B-cell lymphoma	3.5
Cerebellum	74.7	JM1- pre-B-cell lymphoma	3.1
Cerebellum	62.4	Jurkat- T cell leukemia	11.6
NCI-H292- Mucoepidermoid lung carcinoma	45.7	TF-1- Erythroleukemia	13.4
DMS-114- Small cell lung cancer	10.9	HUT 78- T-cell lymphoma	10.0
DMS-79- Small cell lung cancer	100.0	U937- Histiocytic lymphoma	18.2
NCI-H146- Small cell	30.6	KU-812- Myelogenous	6.0

lung cancer		leukemia	
NCI-H526- Small cell lung cancer	57.4	769-P- Clear cell renal carcinoma	11.3
NCI-N417- Small cell lung cancer	15.2	Caki-2- Clear cell renal carcinoma	10.4
NCI-H82- Small cell lung cancer	36.9	SW 839- Clear cell renal carcinoma	2.2
NCI-H157- Squamous cell lung cancer (metastasis)	51.1	G401- Wilms' tumor	6.2
NCI-H1155- Large cell lung cancer	26.6	Hs766T- Pancreatic carcinoma (LN metastasis)	42.9
NCI-H1299- Large cell lung cancer	44.4	CAPAN-1- Pancreatic adenocarcinoma (liver metastasis)	5.0
NCI-H727- Lung carcinoid	47.0	SU86.86- Pancreatic carcinoma (liver metastasis)	28.1
NCI-UMC-11- Lung carcinoid	60.3	BxPC-3- Pancreatic adenocarcinoma	6.3
LX-1- Small cell lung cancer	23.5	HPAC- Pancreatic adenocarcinoma	7.4
Colo-205- Colon cancer	29.5	MIA PaCa-2- Pancreatic carcinoma	3.6
KM12- Colon cancer	24.0	CFPAC-1- Pancreatic ductal adenocarcinoma	40.9
KM20L2- Colon cancer	8.4	PANC-1- Pancreatic epithelioid ductal carcinoma	20.9
NCI-H716- Colon cancer	23.3	T24- Bladder carcinma (transitional cell)	13.1
SW-48- Colon adenocarcinoma	27.0	5637- Bladder carcinoma	11.0
SW1116- Colon adenocarcinoma	10.0	HT-1197- Bladder carcinoma	9.2
LS 174T- Colon adenocarcinoma	9.9	UM-UC-3- Bladder carcinma (transitional cell)	7.2
SW-948- Colon adenocarcinoma	1.1	A204- Rhabdomyosarcoma	7.0
SW-480- Colon adenocarcinoma	8.8	HT-1080- Fibrosarcoma	16.6
NCI-SNU-5- Gastric carcinoma	7.2	MG-63- Osteosarcoma	16.7
KATO III- Gastric carcinoma	32.8	SK-LMS-1- Leiomyosarcoma (vulva)	26.4
NCI-SNU-16- Gastric carcinoma	13.6	SJRH30- Rhabdomyosarcoma (met to bone marrow)	16.8
NCI-SNU-1- Gastric	16.0	A431- Epidermoid carcinoma	9.8

carcinoma			
RF-1- Gastric adenocarcinoma	2.1	WM266-4- Melanoma	12.0
RF-48- Gastric adenocarcinoma	4.0	DU 145- Prostate carcinoma (brain metastasis)	0.1
MKN-45- Gastric carcinoma	28.7	MDA-MB-468- Breast adenocarcinoma	14.7
NCI-N87- Gastric carcinoma	13.3	SCC-4- Squamous cell carcinoma of tongue	0.9
OVCAR-5- Ovarian carcinoma	2.6	SCC-9- Squamous cell carcinoma of tongue	0.3
RL95-2- Uterine carcinoma	7.2	SCC-15- Squamous cell carcinoma of tongue	0.5
HelaS3- Cervical adenocarcinoma	13.4	CAL 27- Squamous cell carcinoma of tongue	21.2

Table CCE. Panel 4D

Tissue Name	Rel. Exp.(%) Ag2075, Run 152787491	Tissue Name	Rel. Exp.(%) Ag2075, Run 152787491
Secondary Th1 act	46.3	HUVEC IL-1beta	25.0
Secondary Th2 act	39.2	HUVEC IFN gamma	33.0
Secondary Tr1 act	31.9	HUVEC TNF alpha + IFN gamma	13.1
Secondary Th1 rest	11.7	HUVEC TNF alpha + IL4	20.7
Secondary Th2 rest	13.9	HUVEC IL-11	20.0
Secondary Tr1 rest	21.6	Lung Microvascular EC none	22.7
Primary Th1 act	30.1	Lung Microvascular EC TNFalpha + IL-1beta	15.0
Primary Th2 act	39.2	Microvascular Dermal EC none	26.8
Primary Tr1 act	54.7	Microvascular Dermal EC TNFalpha + IL-1beta	16.6
Primary Th1 rest	84.1	Bronchial epithelium TNFalpha + IL1beta	4.9
Primary Th2 rest	48.6	Small airway epithelium none	19.9
Primary Tr1 rest	39.0	Small airway epithelium TNFalpha + IL-1beta	72.7
CD45RA CD4 lymphocyte act	21.8	Coronary artery SMC rest	27.9
CD45RO CD4 lymphocyte act	33.0	Coronary artery SMC TNFalpha + IL-1beta	19.6

CD8 lymphocyte act	25.5	Astrocytes rest	26.4
Secondary CD8 lymphocyte rest	21.5	Astrocytes TNFalpha + IL-1beta	13.2
Secondary CD8 lymphocyte act	29.3	KU-812 (Basophil) rest	6.3
CD4 lymphocyte none	12.7	KU-812 (Basophil) PMA/ionomycin	16.0
2ry Th1/Th2/Tr1 _anti-CD95 CH11	25.5	CCD1106 (Keratinocytes) none	46.0
LAK cells rest	26.1	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	4.3
LAK cells IL-2	30.6	Liver cirrhosis	2.7
LAK cells IL-2+IL-12	18.2	Lupus kidney	3.0
LAK cells IL-2+IFN gamma	31.0	NCI-H292 none	76.8
LAK cells IL-2+ IL-18	31.2	NCI-H292 IL-4	94.6
LAK cells PMA/ionomycin	9.5	NCI-H292 IL-9	97.3
NK Cells IL-2 rest	37.4	NCI-H292 IL-13	59.5
Two Way MLR 3 day	24.0	NCI-H292 IFN gamma	51.8
Two Way MLR 5 day	23.0	HPAEC none	23.3
Two Way MLR 7 day	19.6	HPAEC TNF alpha + IL-1 beta	15.8
PBMC rest	11.4	Lung fibroblast none	18.4
PBMC PWM	72.2	Lung fibroblast TNF alpha + IL-1 beta	12.0
PBMC PHA-L	33.9	Lung fibroblast IL-4	35.8
Ramos (B cell) none	19.6	Lung fibroblast IL-9	25.5
Ramos (B cell) ionomycin	100.0	Lung fibroblast IL-13	18.7
B lymphocytes PWM	81.8	Lung fibroblast IFN gamma	38.4
B lymphocytes CD40L and IL-4	42.3	Dermal fibroblast CCD1070 rest	48.0
EOL-1 dbcAMP	23.7	Dermal fibroblast CCD1070 TNF alpha	83.5
EOL-1 dbcAMP PMA/ionomycin	13.5	Dermal fibroblast CCD1070 IL-1 beta	13.6
Dendritic cells none	20.9	Dermal fibroblast IFN gamma	13.1
Dendritic cells LPS	11.5	Dermal fibroblast IL-4	36.6
Dendritic cells anti-CD40	23.2	IBD Colitis 2	1.8
Monocytes rest	19.2	IBD Crohn's	2.4

Monocytes LPS	6.5	Colon	26.8
Macrophages rest	36.1	Lung	21.3
Macrophages LPS	13.3	Thymus	41.5
HUVEC none	37.6	Kidney	24.3
HUVEC starved	58.6		

Panel 1.3D Summary: Ag2075 Highest expression of the CG56870-01 gene is detected in the cerebral cortex (CT=24.2). Thus expression of this gene can be used in distinguishing this sample from other samples in the panel. Furthermore, significant expression of this gene is observed throughout the CNS, including in amygdala, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord. The CG56870-01 gene encodes an Ndr3 homolog which is a putative member of Ndr family. This family consists of proteins from different gene families: Ndr1/RTP/Drg1/NDRG1, Ndr2, and Ndr3 (PFAM: IPR004142). NDRG1 is a cytoplasmic protein involved in stress responses, hormone responses, cell growth, and differentiation. Mutation of this gene was reported to be causative for hereditary motor and sensory neuropathy-Lom. Recently, NDRG4, another member of Ndr family, was shown to be expressed in neurons of the brain and spinal cord. Its expression was markedly decreased in the brain of Alzheimer's disease patient (Zhou et al., 2001). Therefore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

This gene also has moderate levels of expression in adipose, adrenal, thyroid, liver, heart, thyroid and skeletal muscle. Thus, this gene product may be important in the pathogenesis, diagnosis and/or treatment of metabolic and endocrine disease, including Types 1 and 2 diabetes and obesity.

In addition, there appears to be substantial expression in other samples derived from breast cancer cell lines, lung cancer cell lines, renal cancer cell lines and colon cancer cell lines. Thus, therapeutic modulation of this gene could be of benefit in the treatment of breast, lung, renal or colon cancer.

References:

1. Zhou RH, Kokame K, Tsukamoto Y, Yutani C, Kato H, Miyata T. (2001) Characterization of the human NDRG gene family: a newly identified member, NDRG4, is specifically expressed in brain and heart. *Genomics* 73(1):86-97

Ag2075 The expression of this gene appears to be highest in a sample derived from a normal brain tissue. In addition, there appears to be substantial expression in other samples derived from breast cancer cell lines, lung cancer cell lines, renal cancer cell lines and colon cancer cell lines. Thus, the expression of this gene could be used to distinguish normal brain tissue from other samples in the panel. Moreover, therapeutic modulation of this gene could be of benefit in the treatment of breast, lung, renal or colon cancer.

Panel 2.2 Summary: Ag2075 Highest expression of CG56870-01 is detected in breast cancer sample (CT=29.89). Thus expression of this gene can be used in distinguishing this sample from other samples in the panel. In addition, there appears to be substantial expression in other samples derived from breast cancers, kidney cancers and colon cancers. Therefore, therapeutic modulation of this could be of benefit in the treatment of breast, kidney or colon cancer.

Panel 3D Summary: Ag2075 The expression of this gene appears to be highest in a sample derived from a lung cancer cell line (DMS-79)(CT=26.4). In addition, there appears to be substantial expression in other samples derived from pancreatic cancer cell lines, lung cancer cell lines, brain cancer cell lines and cervical cancer cell lines. Thus, the expression of this gene could be used to distinguish DMS-79 cells from other samples in the panel. Moreover, therapeutic modulation of this gene could be of benefit in the treatment of pancreatic, lung, brain or cervical cancer.

Panel 4D Summary: Ag2075 Expression of the CG56870-01 gene is ubiquitous throughout this panel, with highest in samples derived from ionomycin treated Ramos (B cell) cells (CT=26.1). Furthermore, expression of this gene is also detected in PWM treated PBMC cells and PWM treated B lymphocytes. Therefore, therapeutic modulation of the expression or function of this gene may reduce or eliminate the symptoms in patients with autoimmune and inflammatory diseases in which B cells play a part in the initiation or progression of the disease process, such as systemic lupus erythematosus, Crohn's disease, ulcerative colitis, multiple sclerosis, chronic obstructive pulmonary disease, asthma, emphysema, rheumatoid arthritis, or psoriasis.

CD. CG56870-04: N-myc downstream-regulated gene 3

Expression of gene CG56870-04 was assessed using the primer-probe sets Ag5279 and Ag2075, described in Tables CDA and CDB. Results of the RTQ-PCR runs are shown in Tables CDC, CDD, CDE, CDF, CDG, CDH and CDI.

Table CDA. Probe Name Ag5279

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-aggctgtgatggcggact-3'	18	873	650
Probe	TET-5'-ttcagcctgggaagttcaccgaggcc-3'-TAMRA	26	912	651
Reverse	5'-gccgagtcattgctggcagat-3'	20	973	652

Table CDB. Probe Name Ag2075

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-catggatgaacttcaggatggt-3'	22	70	653
Probe	TET-5'-cagctcacagagatcaaaccacttct-3'-TAMRA	26	92	654
Reverse	5'-tgacagtcaaagtcctggaagt-3'	22	141	655

Table CDC. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag5279, Run 230512909	Tissue Name	Rel. Exp.(%) Ag5279, Run 230512909
AD 1 Hippo	7.7	Control (Path) 3 Temporal Ctx	1.0
AD 2 Hippo	8.4	Control (Path) 4 Temporal Ctx	13.2
AD 3 Hippo	3.4	AD 1 Occipital Ctx	7.2
AD 4 Hippo	2.8	AD 2 Occipital Ctx (Missing)	0.0
AD 5 hippo	100.0	AD 3 Occipital Ctx	2.1
AD 6 Hippo	32.8	AD 4 Occipital Ctx	13.1
Control 2 Hippo	32.3	AD 5 Occipital Ctx	15.6
Control 4 Hippo	2.7	AD 6 Occipital Ctx	54.7
Control (Path) 3 Hippo	1.2	Control 1 Occipital Ctx	1.1
AD 1 Temporal Ctx	6.4	Control 2 Occipital Ctx	81.2
AD 2 Temporal Ctx	17.1	Control 3 Occipital Ctx	8.1
AD 3 Temporal Ctx	2.3	Control 4 Occipital Ctx	2.5
AD 4 Temporal Ctx	8.7	Control (Path) 1 Occipital Ctx	66.0
AD 5 Inf Temporal Ctx	79.0	Control (Path) 2 Occipital Ctx	5.6

AD 5 SupTemporal Ctx	6.4	Control (Path) 3 Occipital Ctx	1.5
AD 6 Inf Temporal Ctx	25.7	Control (Path) 4 Occipital Ctx	7.6
AD 6 Sup Temporal Ctx	24.1	Control 1 Parietal Ctx	2.4
Control 1 Temporal Ctx	2.0	Control 2 Parietal Ctx	10.7
Control 2 Temporal Ctx	41.2	Control 3 Parietal Ctx	16.6
Control 3 Temporal Ctx	4.6	Control (Path) 1 Parietal Ctx	75.3
Control 4 Temporal Ctx	2.7	Control (Path) 2 Parietal Ctx	13.7
Control (Path) 1 Temporal Ctx	35.4	Control (Path) 3 Parietal Ctx	1.6
Control (Path) 2 Temporal Ctx	27.7	Control (Path) 4 Parietal Ctx	19.3

Table CDD. General_screening_panel_v1.5

Tissue Name	Rel. Exp.(%) Ag5279, Run 230509998	Tissue Name	Rel. Exp.(%) Ag5279, Run 230509998
Adipose	1.3	Renal ca. TK-10	9.2
Melanoma* Hs688(A).T	7.6	Bladder	2.4
Melanoma* Hs688(B).T	8.0	Gastric ca. (liver met.) NCI-N87	8.7
Melanoma* M14	12.2	Gastric ca. KATO III	21.8
Melanoma* LOXIMVI	13.8	Colon ca. SW-948	4.6
Melanoma* SK-MEL-5	8.2	Colon ca. SW480	14.1
Squamous cell carcinoma SCC-4	6.5	Colon ca.* (SW480 met) SW620	10.4
Testis Pool	8.2	Colon ca. HT29	12.3
Prostate ca.* (bone met) PC-3	2.3	Colon ca. HCT-116	12.2
Prostate Pool	6.2	Colon ca. CaCo-2	17.8
Placenta	3.5	Colon cancer tissue	4.9
Uterus Pool	1.4	Colon ca. SW1116	2.6
Ovarian ca. OVCAR-3	8.8	Colon ca. Colo-205	7.3
Ovarian ca. SK-OV-3	20.4	Colon ca. SW-48	5.9

Ovarian ca. OVCAR-4	5.6	Colon Pool	5.1
Ovarian ca. OVCAR-5	10.9	Small Intestine Pool	3.9
Ovarian ca. IGROV-1	6.0	Stomach Pool	2.3
Ovarian ca. OVCAR-8	5.5	Bone Marrow Pool	1.5
Ovary	5.7	Fetal Heart	7.5
Breast ca. MCF-7	5.0	Heart Pool	3.3
Breast ca. MDA-MB-231	23.0	Lymph Node Pool	5.1
Breast ca. BT 549	21.9	Fetal Skeletal Muscle	3.1
Breast ca. T47D	10.6	Skeletal Muscle Pool	4.0
Breast ca. MDA-N	5.8	Spleen Pool	2.2
Breast Pool	5.9	Thymus Pool	2.9
Trachea	5.0	CNS cancer (glio/astro) U87-MG	20.4
Lung	2.5	CNS cancer (glio/astro) U-118-MG	16.8
Fetal Lung	8.7	CNS cancer (neuro;met) SK-N-AS	10.7
Lung ca. NCI-N417	3.7	CNS cancer (astro) SF-539	7.0
Lung ca. LX-1	12.1	CNS cancer (astro) SNB-75	21.3
Lung ca. NCI-H146	5.8	CNS cancer (glio) SNB-19	5.8
Lung ca. SHP-77	7.9	CNS cancer (glio) SF-295	12.2
Lung ca. A549	14.1	Brain (Amygdala) Pool	19.3
Lung ca. NCI-H526	5.1	Brain (cerebellum)	100.0
Lung ca. NCI-H23	11.2	Brain (fetal)	20.0
Lung ca. NCI-H460	2.9	Brain (Hippocampus) Pool	17.4
Lung ca. HOP-62	4.6	Cerebral Cortex Pool	23.7
Lung ca. NCI-H522	13.6	Brain (Substantia nigra) Pool	17.9
Liver	0.5	Brain (Thalamus) Pool	34.2
Fetal Liver	3.2	Brain (whole)	46.3
Liver ca. HepG2	5.3	Spinal Cord Pool	9.5
Kidney Pool	7.1	Adrenal Gland	11.8
Fetal Kidney	5.7	Pituitary gland Pool	2.9
Renal ca. 786-0	6.3	Salivary Gland	3.5

Renal ca. A498	11.0	Thyroid (female)	2.0
Renal ca. ACHN	6.0	Pancreatic ca. CAPAN2	5.6
Renal ca. UO-31	8.0	Pancreas Pool	6.2

Table CDE. Panel 1.3D

Tissue Name	Rel. Exp.(%) Ag2075, Run 152355202	Tissue Name	Rel. Exp.(%) Ag2075, Run 152355202
Liver adenocarcinoma	11.9	Kidney (fetal)	1.4
Pancreas	0.8	Renal ca. 786-0	3.5
Pancreatic ca. CAPAN 2	1.6	Renal ca. A498	12.9
Adrenal gland	2.4	Renal ca. RXF 393	1.5
Thyroid	1.8	Renal ca. ACHN	1.7
Salivary gland	1.2	Renal ca. UO-31	6.8
Pituitary gland	2.4	Renal ca. TK-10	2.8
Brain (fetal)	3.2	Liver	0.4
Brain (whole)	25.2	Liver (fetal)	0.8
Brain (amygdala)	14.1	Liver ca. (hepatoblast) HepG2	6.7
Brain (cerebellum)	10.8	Lung	2.1
Brain (hippocampus)	39.8	Lung (fetal)	3.2
Brain (substantia nigra)	2.7	Lung ca. (small cell) LX-1	4.1
Brain (thalamus)	12.4	Lung ca. (small cell) NCI-H69	3.8
Cerebral Cortex	100.0	Lung ca. (s.cell var.) SHP-77	3.8
Spinal cord	3.5	Lung ca. (large cell)NCI-H460	0.6
glio/astro U87-MG	6.4	Lung ca. (non-sm. cell) A549	3.0
glio/astro U-118-MG	10.4	Lung ca. (non-s.cell) NCI-H23	7.7
astrocytoma SW1783	5.1	Lung ca. (non-s.cell) HGP-62	3.1
neuro*; met SK-N-AS	6.2	Lung ca. (non-s.cl) NCI-H522	6.3
astrocytoma SF-539	5.4	Lung ca. (squam.) SW 900	1.4
astrocytoma SNB-75	6.7	Lung ca. (squam.) NCI-H596	1.4
glioma SNB-19	3.1	Mammary gland	2.4
glioma U251	2.0	Breast ca.* (pl.ef)	1.8

		MCF-7	
glioma SF-295	3.4	Breast ca.* (pl.ef) MDA-MB-231	11.6
Heart (fetal)	6.7	Breast ca.* (pl.ef) T47D	9.0
Heart	1.4	Breast ca. BT-549	4.8
Skeletal muscle (fetal)	18.0	Breast ca. MDA-N	4.2
Skeletal muscle	0.7	Ovary	13.4
Bone marrow	0.9	Ovarian ca. OVCAR-3	1.8
Thymus	0.9	Ovarian ca. OVCAR-4	1.6
Spleen	3.7	Ovarian ca. OVCAR-5	1.8
Lymph node	1.9	Ovarian ca. OVCAR-8	4.9
Colorectal	3.3	Ovarian ca. IGROV-1	1.6
Stomach	2.7	Ovarian ca.* (ascites) SK-OV-3	5.8
Small intestine	2.5	Uterus	2.4
Colon ca. SW480	10.4	Placenta	1.2
Colon ca.* SW620(SW480 met)	3.7	Prostate	6.0
Colon ca. HT29	4.6	Prostate ca.* (bone met)PC-3	4.5
Colon ca. HCT-116	3.6	Testis	1.7
Colon ca. CaCo-2	10.3	Melanoma Hs688(A).T	3.8
Colon ca. tissue(ODO3866)	3.2	Melanoma* (met) Hs688(B).T	4.4
Colon ca. HCC-2998	2.6	Melanoma UACC-62	1.4
Gastric ca.* (liver met) NCI-N87	3.1	Melanoma M14	1.8
Bladder	0.8	Melanoma LOX IMVI	3.3
Trachea	2.0	Melanoma* (met) SK-MEL-5	2.4
Kidney	1.3	Adipose	1.2

Table CDF. Panel 2.2

Tissue Name	Rel. Exp.(%) Ag2075, Run 174255357	Tissue Name	Rel. Exp.(%) Ag2075, Run 174255357
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Normal Colon	27.7	Kidney Margin (OD04348)	46.3
Colon cancer (OD06064)	52.9	Kidney malignant cancer (OD06204B)	19.2
Colon Margin (OD06064)	30.1	Kidney normal adjacent tissue (OD06204E)	14.3
Colon cancer (OD06159)	5.5	Kidney Cancer (OD04450-01)	66.0
Colon Margin (OD06159)	21.0	Kidney Margin (OD04450-03)	19.8
Colon cancer (OD06297-04)	22.2	Kidney Cancer 8120613	3.0
Colon Margin (OD06297-05)	41.8	Kidney Margin 8120614	11.0
CC Gr.2 ascend colon (ODO3921)	4.0	Kidney Cancer 9010320	6.8
CC Margin (ODO3921)	6.7	Kidney Margin 9010321	9.7
Colon cancer metastasis (OD06104)	11.1	Kidney Cancer 8120607	35.6
Lung Margin (OD06104)	42.6	Kidney Margin 8120608	13.7
Colon mets to lung (OD04451-01)	17.8	Normal Uterus	59.5
Lung Margin (OD04451-02)	9.3	Uterine Cancer 064011	9.7
Normal Prostate	51.4	Normal Thyroid	8.8
Prostate Cancer (OD04410)	23.0	Thyroid Cancer 064010	11.2
Prostate Margin (OD04410)	19.3	Thyroid Cancer A302152	17.9
Normal Ovary	22.8	Thyroid Margin A302153	5.5
Ovarian cancer (OD06283-03)	9.9	Normal Breast	33.2
Ovarian Margin (OD06283-07)	17.1	Breast Cancer (OD04566)	8.5
Ovarian Cancer 064008	18.0	Breast Cancer 1024	36.1
Ovarian cancer (OD06145)	6.6	Breast Cancer (OD04590-01)	18.4
Ovarian Margin (OD06145)	12.5	Breast Cancer Mets (OD04590-03)	31.9
Ovarian cancer (OD06455-03)	14.7	Breast Cancer Metastasis (OD04655-05)	45.4

Ovarian Margin (OD06455-07)	21.8	Breast Cancer 064006	11.5
Normal Lung	21.9	Breast Cancer 9100266	20.9
Invasive poor diff. lung adeno (ODO4945-01)	17.6	Breast Margin 9100265	35.1
Lung Margin (ODO4945-03)	12.2	Breast Cancer A209073	9.7
Lung Malignant Cancer (OD03126)	8.7	Breast Margin A2090734	22.2
Lung Margin (OD03126)	7.4	Breast cancer (OD06083)	100.0
Lung Cancer (OD05014A)	9.9	Breast cancer node metastasis (OD06083)	63.7
Lung Margin (OD05014B)	21.8	Normal Liver	9.9
Lung cancer (OD06081)	5.1	Liver Cancer 1026	5.6
Lung Margin (OD06081)	7.9	Liver Cancer 1025	13.5
Lung Cancer (OD04237-01)	17.4	Liver Cancer 6004-T	4.8
Lung Margin (OD04237-02)	24.0	Liver Tissue 6004-N	9.3
Ocular Melanoma Metastasis	9.7	Liver Cancer 6005-T	15.7
Ocular Melanoma Margin (Liver)	4.6	Liver Tissue 6005-N	20.4
Melanoma Metastasis	19.8	Liver Cancer 064003	10.7
Melanoma Margin (Lung)	21.6	Normal Bladder	8.0
Normal Kidney	11.0	Bladder Cancer 1023	10.5
Kidney Ca, Nuclear grade 2 (OD04338)	37.6	Bladder Cancer A302173	17.3
Kidney Margin (OD04338)	22.1	Normal Stomach	37.9
Kidney Ca Nuclear grade 1/2 (OD04339)	21.6	Gastric Cancer 9060397	11.1
Kidney Margin (OD04339)	12.9	Stomach Margin 9060396	20.6
Kidney Ca, Clear cell type (OD04340)	6.5	Gastric Cancer 9060395	22.7
Kidney Margin (OD04340)	18.4	Stomach Margin 9060394	36.1
Kidney Ca, Nuclear grade 3 (OD04348)	12.9	Gastric Cancer 064005	8.1

Table CDG. Panel 3D

Tissue Name	Rel. Exp.(%) Ag2075, Run 164750734	Tissue Name	Rel. Exp.(%) Ag2075, Run 164750734
Daoy- Medulloblastoma	6.7	Ca Ski- Cervical epidermoid carcinoma (metastasis)	50.3
TE671- Medulloblastoma	9.0	ES-2- Ovarian clear cell carcinoma	13.9
D283 Med- Medulloblastoma	35.4	Ramos- Stimulated with PMA/ionomycin 6h	2.7
PFSK-1- Primitive Neuroectodermal	15.4	Ramos- Stimulated with PMA/ionomycin 14h	3.3
XF-498- CNS	4.4	MEG-01- Chronic myelogenous leukemia (megakaryoblast)	3.4
SNB-78- Glioma	23.3	Raji- Burkitt's lymphoma	3.7
SF-268- Glioblastoma	13.6	Daudi- Burkitt's lymphoma	6.5
T98G- Glioblastoma	18.6	U266- B-cell plasmacytoma	8.4
SK-N-SH- Neuroblastoma (metastasis)	17.0	CA46- Burkitt's lymphoma	7.2
SF-295- Glioblastoma	8.4	RL- non-Hodgkin's B-cell lymphoma	3.5
Cerebellum	74.7	JM1- pre-B-cell lymphoma	3.1
Cerebellum	62.4	Jurkat- T cell leukemia	11.6
NCI-H292- Mucoepidermoid lung carcinoma	45.7	TF-1- Erythroleukemia	13.4
DMS-114- Small cell lung cancer	10.9	HUT 78- T-cell lymphoma	10.0
DMS-79- Small cell lung cancer	100.0	U937- Histiocytic lymphoma	18.2
NCI-H146- Small cell lung cancer	30.6	KU-812- Myelogenous leukemia	6.0
NCI-H526- Small cell lung cancer	57.4	769-P- Clear cell renal carcinoma	11.3
NCI-N417- Small cell lung cancer	15.2	Caki-2- Clear cell renal carcinoma	10.4
NCI-H82- Small cell lung cancer	36.9	SW 839- Clear cell renal carcinoma	2.2
NCI-H157- Squamous cell lung cancer (metastasis)	51.1	G401- Wilms' tumor	6.2
NCI-H1155- Large cell	26.6	Hs766T- Pancreatic	42.9

lung cancer		carcinoma (LN metastasis)	
NCI-H1299- Large cell lung cancer	44.4	CAPAN-1- Pancreatic adenocarcinoma (liver metastasis)	5.0
NCI-H727- Lung carcinoid	47.0	SU86.86- Pancreatic carcinoma (liver metastasis)	28.1
NCI-UMC-11- Lung carcinoid	60.3	BxPC-3- Pancreatic adenocarcinoma	6.3
LX-1- Small cell lung cancer	23.5	HPAC- Pancreatic adenocarcinoma	7.4
Colo-205- Colon cancer	29.5	MIA PaCa-2- Pancreatic carcinoma	3.6
KM12- Colon cancer	24.0	CFPAC-1- Pancreatic ductal adenocarcinoma	40.9
KM20L2- Colon cancer	8.4	PANC-1- Pancreatic epithelioid ductal carcinoma	20.9
NCI-H716- Colon cancer	23.3	T24- Bladder carcinma (transitional cell)	13.1
SW-48- Colon adenocarcinoma	27.0	5637- Bladder carcinoma	11.0
SW1116- Colon adenocarcinoma	10.0	HT-1197- Bladder carcinoma	9.2
LS 174T- Colon adenocarcinoma	9.9	UM-UC-3- Bladder carcinma (transitional cell)	7.2
SW-948- Colon adenocarcinoma	1.1	A204- Rhabdomyosarcoma	7.0
SW-480- Colon adenocarcinoma	8.8	HT-1080- Fibrosarcoma	16.6
NCI-SNU-5- Gastric carcinoma	7.2	MG-63- Osteosarcoma	16.7
KATO III- Gastric carcinoma	32.8	SK-LMS-1- Leiomyosarcoma (vulva)	26.4
NCI-SNU-16- Gastric carcinoma	13.6	SJRH30- Rhabdomyosarcoma (met to bone marrow)	16.8
NCI-SNU-1- Gastric carcinoma	16.0	A431- Epidermoid carcinoma	9.8
RF-1- Gastric adenocarcinoma	2.1	WM266-4- Melanoma	12.0
RF-48- Gastric adenocarcinoma	4.0	DU 145- Prostate carcinoma (brain metastasis)	0.1
MKN-45- Gastric carcinoma	28.7	MDA-MB-468- Breast adenocarcinoma	14.7
NCI-N87- Gastric carcinoma	13.3	SCC-4- Squamous cell carcinoma of tongue	0.9
OVCAR-5- Ovarian carcinoma	2.6	SCC-9- Squamous cell carcinoma of tongue	0.3

RL95-2- Uterine carcinoma	7.2	SCC-15- Squamous cell carcinoma of tongue	0.5
HelaS3- Cervical adenocarcinoma	13.4	CAL 27- Squamous cell carcinoma of tongue	21.2

Table CDH. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag5279, Run 230472927	Tissue Name	Rel. Exp.(%) Ag5279, Run 230472927
Secondary Th1 act	59.0	HUVEC IL-1beta	41.5
Secondary Th2 act	91.4	HUVEC IFN gamma	71.7
Secondary Tr1 act	27.5	HUVEC TNF alpha + IFN gamma	17.4
Secondary Th1 rest	7.5	HUVEC TNF alpha + IL4	20.7
Secondary Th2 rest	8.4	HUVEC IL-11	32.3
Secondary Tr1 rest	2.6	Lung Microvascular EC none	57.4
Primary Th1 act	26.8	Lung Microvascular EC TNFalpha + IL-1beta	14.6
Primary Th2 act	55.1	Microvascular Dermal EC none	10.9
Primary Tr1 act	55.5	Microvascular Dermal EC TNFalpha + IL-1beta	13.2
Primary Th1 rest	3.2	Bronchial epithelium TNFalpha + IL1beta	17.4
Primary Th2 rest	13.7	Small airway epithelium none	18.8
Primary Tr1 rest	7.6	Small airway epithelium TNFalpha + IL-1beta	56.3
CD45RA CD4 lymphocyte act	31.9	Coronary artery SMC rest	31.9
CD45RO CD4 lymphocyte act	48.3	Coronary artery SMC TNFalpha + IL-1beta	37.1
CD8 lymphocyte act	21.2	Astrocytes rest	28.3
Secondary CD8 lymphocyte rest	36.1	Astrocytes TNFalpha + IL-1beta	15.8
Secondary CD8 lymphocyte act	8.0	KU-812 (Basophil) rest	15.2
CD4 lymphocyte none	8.4	KU-812 (Basophil) PMA/ionomycin	17.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	8.9	CCD1106 (Keratinocytes) none	71.2
LAK cells rest	26.1	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	42.0

LAK cells IL-2	16.3	Liver cirrhosis	15.5
LAK cells IL-2+IL-12	2.0	NCI-H292 none	45.4
LAK cells IL-2+IFN gamma	12.5	NCI-H292 IL-4	63.7
LAK cells IL-2+ IL-18	7.5	NCI-H292 IL-9	70.7
LAK cells PMA/ionomycin	21.9	NCI-H292 IL-13	99.3
NK Cells IL-2 rest	44.4	NCI-H292 IFN gamma	45.4
Two Way MLR 3 day	21.9	HPAEC none	25.9
Two Way MLR 5 day	13.5	HPAEC TNF alpha + IL-1 beta	34.9
Two Way MLR 7 day	11.3	Lung fibroblast none	37.9
PBMC rest	11.0	Lung fibroblast TNF alpha + IL-1 beta	21.2
PBMC PWM	4.5	Lung fibroblast IL-4	31.6
PBMC PHA-L	18.4	Lung fibroblast IL-9	36.3
Ramos (B cell) none	14.0	Lung fibroblast IL-13	9.0
Ramos (B cell) ionomycin	42.9	Lung fibroblast IFN gamma	58.6
B lymphocytes PWM	18.9	Dermal fibroblast CCD1070 rest	43.2
B lymphocytes CD40L and IL-4	31.0	Dermal fibroblast CCD1070 TNF alpha	100.0
EOL-1 dbcAMP	37.9	Dermal fibroblast CCD1070 IL-1 beta	23.5
EOL-1 dbcAMP PMA/ionomycin	14.7	Dermal fibroblast IFN gamma	31.4
Dendritic cells none	26.2	Dermal fibroblast IL-4	45.4
Dendritic cells LPS	13.2	Dermal Fibroblasts rest	61.6
Dendritic cells anti-CD40	17.0	Neutrophils TNFa+LPS	4.2
Monocytes rest	11.6	Neutrophils rest	31.4
Monocytes LPS	8.5	Colon	1.0
Macrophages rest	12.9	Lung	1.6
Macrophages LPS	2.6	Thymus	4.5
HUVEC none	36.1	Kidney	32.5
HUVEC starved	36.9	..	

Table CDI. Panel 4D

Tissue Name	Rel. Exp.(%) Ag2075, Run 152787491	Tissue Name	Rel. Exp.(%) Ag2075, Run 152787491
Secondary Th1 act	46.3	HUVEC IL-1beta	25.0

Secondary Th2 act	39.2	HUVEC IFN gamma	33.0
Secondary Tr1 act	31.9	HUVEC TNF alpha + IFN gamma	13.1
Secondary Th1 rest	11.7	HUVEC TNF alpha + IL4	20.7
Secondary Th2 rest	13.9	HUVEC IL-11	20.0
Secondary Tr1 rest	21.6	Lung Microvascular EC none	22.7
Primary Th1 act	30.1	Lung Microvascular EC TNFalpha + IL-1beta	15.0
Primary Th2 act	39.2	Microvascular Dermal EC none	26.8
Primary Tr1 act	54.7	Microvascular Dermal EC TNFalpha + IL-1beta	16.6
Primary Th1 rest	84.1	Bronchial epithelium TNFalpha + IL1beta	4.9
Primary Th2 rest	48.6	Small airway epithelium none	19.9
Primary Tr1 rest	39.0	Small airway epithelium TNFalpha + IL-1beta	72.7
CD45RA CD4 lymphocyte act	21.8	Coronary artery SMC rest	27.9
CD45RO CD4 lymphocyte act	33.0	Coronary artery SMC TNFalpha + IL-1beta	19.6
CD8 lymphocyte act	25.5	Astrocytes rest	26.4
Secondary CD8 lymphocyte rest	21.5	Astrocytes TNFalpha + IL-1beta	13.2
Secondary CD8 lymphocyte act	29.3	KU-812 (Basophil) rest	6.3
CD4 lymphocyte none	12.7	KU-812 (Basophil) PMA/ionomycin	16.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	25.5	CCD1106 (Keratinocytes) none	46.0
LAK cells rest	26.1	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	4.3
LAK cells IL-2	30.6	Liver cirrhosis	2.7
LAK cells IL-2+IL-12	18.2	Lupus kidney	3.0
LAK cells IL-2+IFN gamma	31.0	NCI-H292 none	76.8
LAK cells IL-2+ IL-18	31.2	NCI-H292 IL-4	94.6
LAK cells PMA/ionomycin	9.5	NCI-H292 IL-9	97.3
NK Cells IL-2 rest	37.4	NCI-H292 IL-13	59.5
Two Way MLR 3 day	24.0	NCI-H292 IFN gamma	51.8
Two Way MLR 5 day	23.0	HPAEC none	23.3
Two Way MLR 7 day	19.6	HPAEC TNF alpha + IL-1	15.8

		beta	
PBMC rest	11.4	Lung fibroblast none	18.4
PBMC PWM	72.2	Lung fibroblast TNF alpha + IL-1 beta	12.0
PBMC PHA-L	33.9	Lung fibroblast IL-4	35.8
Ramos (B cell) none	19.6	Lung fibroblast IL-9	25.5
Ramos (B cell) ionomycin	100.0	Lung fibroblast IL-13	18.7
B lymphocytes PWM	81.8	Lung fibroblast IFN gamma	38.4
B lymphocytes CD40L and IL-4	42.3	Dermal fibroblast CCD1070 rest	48.0
EOL-1 dbcAMP	23.7	Dermal fibroblast CCD1070 TNF alpha	83.5
EOL-1 dbcAMP PMA/ionomycin	13.5	Dermal fibroblast CCD1070 IL-1 beta	13.6
Dendritic cells none	20.9	Dermal fibroblast IFN gamma	13.1
Dendritic cells LPS	11.5	Dermal fibroblast IL-4	36.6
Dendritic cells anti-CD40	23.2	IBD Colitis 2	1.8
Monocytes rest	19.2	IBD Crohn's	2.4
Monocytes LPS	6.5	Colon	26.8
Macrophages rest	36.1	Lung	21.3
Macrophages LPS	13.3	Thymus	41.5
HUVEC none	37.6	Kidney	24.3
HUVEC starved	58.6		

CNS_neurodegeneration_v1.0 Summary: Ag5279 This panel confirms the expression of the CG56870-04 gene at low levels in the brain in an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. Please see Panel 1.5 for a discussion of the potential utility of this gene in treatment of central nervous system disorders.

General_screening_panel_v1.5 Summary: Ag5279 Highest expression of the CG56870-01 is detected in cerebral cortex (CT=25.02). Thus, expression of this gene can be used in distinguishing this sample from other samples in the panel. Furthermore, significant expression of this gene is observed throughout the CNS, including in amygdala, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord. The CG56870-01 gene encodes a Ndr3 protein homolog. The Ndr family is comprised of members from different gene families:

Ndr1/RTP/Drg1/NDRG1, Ndr2, and Ndr3 (PFAM: IPR004142). NDRG1 is a cytoplasmic protein involved in stress responses, hormone responses, cell growth, and differentiation. Mutation of this gene was reported to be causative for hereditary motor and sensory neuropathy-Lom. Recently, NDRG4, another member of Ndr family, was shown to be expressed in neurons of the brain and spinal cord. Its expression was markedly decreased in the brain of Alzheimer's disease patient (Zhou et al., 2001). Therefore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

Among metabolic tissues, this gene is moderately expressed in adipose, adrenal, heart, thyroid, liver, pancreas, pituitary, and skeletal muscle. Thus, this gene product may be important for the pathogenesis, diagnosis, and/or treatment of metabolic and endocrine disease, including Types 1 and 2 diabetes and obesity.

In addition, there appears to be substantial expression in other samples derived from brain cancer cell lines, colon cancer cell lines, breast cancer cell lines and ovarian cancer cell lines. Moreover, therapeutic modulation of this gene could be of benefit in the treatment of brain, colon, breast or ovarian cancer.

References:

1. Zhou RH, Kokame K, Tsukamoto Y, Yutani C, Kato H, Miyata T. (2001) Characterization of the human NDRG gene family: a newly identified member, NDRG4, is specifically expressed in brain and heart. *Genomics* 73(1):86-97

Panel 1.3D Summary: Ag2075 Highest expression of the CG56870-01 gene is detected in the cerebral cortex (CT=24.2). This expression is consistent with expression in Panel 1.5. Please see that panel for discussion of utility of this gene in the central nervous system.

This gene also has moderate levels of expression in adipose, adrenal, thyroid, liver, heart, thyroid and skeletal muscle. Thus, this gene product may be important in the pathogenesis, diagnosis and/or treatment of metabolic and endocrine disease, including Types 1 and 2 diabetes and obesity.

In addition, there appears to be substantial expression in other samples derived from breast cancer cell lines, lung cancer cell lines, renal cancer cell lines and colon cancer cell

lines. Thus, therapeutic modulation of this gene could be of benefit in the treatment of breast, lung, renal or colon cancer.

Panel 2.2 Summary: Ag2075 Highest expression of CG56870-01 is detected in breast cancer sample (CT=29.89). Thus expression of this gene can be used in distinguishing this sample from other samples in the panel. In addition, there appears to be substantial expression in other samples derived from breast cancers, kidney cancers and colon cancers. Therefore, therapeutic modulation of this gene could be of benefit in the treatment of breast, kidney or colon cancer.

Panel 3D Summary: Ag2075 The expression of this gene appears to be highest in a sample derived from a lung cancer cell line (DMS-79)(CT=26.4). In addition, there appears to be substantial expression in other samples derived from pancreatic cancer cell lines, lung cancer cell lines, brain cancer cell lines and cervical cancer cell lines. Thus, the expression of this gene could be used to distinguish DMS-79 cells from other samples in the panel. Moreover, therapeutic modulation of this gene could be of benefit in the treatment of pancreatic, lung, brain or cervical cancer.

Panel 4.1D Summary: Ag5279 Expression of the CG56870-01 gene is highest in samples derived from TNF alpha treated dermal fibroblast CCD1070 cells (CT=30.6). Expression of this gene is also prominent in activated secondary and primary Th1, Th2 and Tr1 cells when compared expression in the corresponding resting cell lines. Thus, this gene may be involved in T lymphocyte function. Therefore, therapeutic modulation of the expression or function of this gene may be as anti-inflammatory therapeutics for T cell-mediated autoimmune and inflammatory diseases, such as asthma, arthritis, psoriasis, IBD, and lupus.

Panel 4D Summary: Ag2075 Expression of the CG56870-01 gene is ubiquitous throughout this panel, with highest in samples derived from ionomycin treated Ramos (B cell) cells (CT=26.1). Furthermore, expression of this gene is also detected in PWM treated PBMC cells and PWM treated B lymphocytes. Therefore, therapeutic modulation of the expression or function of this gene may reduce or eliminate the symptoms in patients with autoimmune and inflammatory diseases in which B cells play a part in the initiation or progression of the disease process, such as systemic lupus erythematosus, Crohn's disease, ulcerative colitis, multiple sclerosis, chronic obstructive pulmonary disease, asthma, emphysema, rheumatoid arthritis, or psoriasis.

CE. CG56870-05: N-myc downstream-regulated gene 3

Expression of gene CG56870-05 was assessed using the primer-probe set Ag5265, described in Table CEA. Results of the RTQ-PCR runs are shown in Tables CEB and CEC.

Table CEA. Probe Name Ag5265

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-tggtcagctcacagagatcaaa-3'	22	18	656
Probe	TET-5'-caagaaacttcaggactttgactgtca-3'-TAMRA	28	65	657
Reverse	5'-catccattgtgggggtactga-3'	20	96	658

Table CEB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag5265, Run 230512714	Tissue Name	Rel. Exp.(%) Ag5265, Run 230512714
AD 1 Hippo	7.2	Control (Path) 3 Temporal Ctx	2.4
AD 2 Hippo	15.2	Control (Path) 4 Temporal Ctx	10.3
AD 3 Hippo	2.0	AD 1 Occipital Ctx	11.5
AD 4 Hippo	3.3	AD 2 Occipital Ctx (Missing)	0.0
AD 5 Hippo	59.9	AD 3 Occipital Ctx	7.0
AD 6 Hippo	22.1	AD 4 Occipital Ctx	6.9
Control 2 Hippo	14.5	AD 5 Occipital Ctx	54.7
Control 4 Hippo	2.6	AD 6 Occipital Ctx	12.2
Control (Path) 3 Hippo	3.9	Control 1 Occipital Ctx	1.2
AD 1 Temporal Ctx	12.7	Control 2 Occipital Ctx	60.3
AD 2 Temporal Ctx	16.0	Control 3 Occipital Ctx	8.2
AD 3 Temporal Ctx	5.5	Control 4 Occipital Ctx	1.7
AD 4 Temporal Ctx	13.9	Control (Path) 1 Occipital Ctx	53.6
AD 5 Inf Temporal Ctx	64.6	Control (Path) 2 Occipital Ctx	5.9
AD 5 Sup Temporal Ctx	28.9	Control (Path) 3 Occipital Ctx	2.2
AD 6 Inf Temporal Ctx	27.0	Control (Path) 4 Occipital Ctx	5.5
AD 6 Sup Temporal	100.0	Control 1 Parietal	3.0

Ctx		Ctx	
Control 1 Temporal Ctx	2.6	Control 2 Parietal Ctx	19.6
Control 2 Temporal Ctx	38.2	Control 3 Parietal Ctx	18.8
Control 3 Temporal Ctx	9.7	Control (Path) 1 Parietal Ctx	56.6
Control 3 Temporal Ctx	1.5	Control (Path) 2 Parietal Ctx	14.2
Control (Path) 1 Temporal Ctx	31.4	Control (Path) 3 Parietal Ctx	2.6
Control (Path) 2 Temporal Ctx	18.3	Control (Path) 4 Parietal Ctx	25.0

Table CEC. General_screening_panel_v1.5

Tissue Name	Rel. Exp.(%) Ag5265, Run 232936652	Tissue Name	Rel. Exp.(%) Ag5265, Run 232936652
Adipose	1.1	Renal ca. TK-10	14.8
Melanoma* Hs688(A).T	7.9	Bladder	2.5
Melanoma* Hs688(B).T	10.1	Gastric ca. (liver met.) NCI-N87	7.3
Melanoma* M14	12.4	Gastric ca. KATO III	17.8
Melanoma* LOXIMVI	13.7	Colon ca. SW-948	1.8
Melanoma* SK- MEL-5	9.9	Colon ca. SW480	16.0
Squamous cell carcinoma SCC-4	8.3	Colon ca.* (SW480 met) SW620	8.2
Testis Pool	2.2	Colon ca. HT29	6.7
Prostate ca.* (bone met) PC-3	18.0	Colon ca. HCT-116	15.8
Prostate Pool	4.4	Colon ca. CaCo-2	25.5
Placenta	2.1	Colon cancer tissue	2.5
Uterus Pool	1.9	Colon ca. SW1116	2.3
Ovarian ca. OVCAR-3	9.0	Colon ca. Colo-205	4.8
Ovarian ca. SK-OV- 3	16.0	Colon ca. SW-48	5.1
Ovarian ca. OVCAR-4	4.5	Colon Pool	2.8
Ovarian ca. OVCAR-5	10.4	Small Intestine Pool	2.4
Ovarian ca. IGROV-	12.0	Stomach Pool	1.8

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Ovarian ca. OVCAR-8	4.5	Bone Marrow Pool	1.2
Ovary	2.8	Fetal Heart	2.3
Breast ca. MCF-7	4.9	Heart Pool	1.5
Breast ca. MDA-MB-231	30.1	Lymph Node Pool	3.0
Breast ca. BT 549	18.9	Fetal Skeletal Muscle	0.9
Breast ca. T47D	4.0	Skeletal Muscle Pool	1.8
Breast ca. MDA-N	8.4	Spleen Pool	2.2
Breast Pool	3.6	Thymus Pool	1.9
Trachea	3.2	CNS cancer (glio/astro) U87-MG	18.3
Lung	1.7	CNS cancer (glio/astro) U-118-MG	19.5
Fetal Lung	4.8	CNS cancer (neuro;met) SK-N-AS	8.4
Lung ca. NCI-N417	2.0	CNS cancer (astro) SF-539	8.8
Lung ca. LX-1	8.5	CNS cancer (astro) SNB-75	29.1
Lung ca. NCI-H146	9.2	CNS cancer (glio) SNB-19	10.9
Lung ca. SHP-77	8.2	CNS cancer (glio) SF-295	17.2
Lung ca. A549	15.2	Brain (Amygdala) Pool	14.0
Lung ca. NCI-H526	3.2	Brain (cerebellum)	100.0
Lung ca. NCI-H23	16.2	Brain (fetal)	10.7
Lung ca. NCI-H460	2.7	Brain (Hippocampus) Pool	11.4
Lung ca. HOP-62	5.6	Cerebral Cortex Pool	15.5
Lung ca. NCI-H522	13.0	Brain (Substantia nigra) Pool	14.7
Liver	0.9	Brain (Thalamus) Pool	17.9
Fetal Liver	2.4	Brain (whole)	25.9
Liver ca. HepG2	6.2	Spinal Cord Pool	9.0
Kidney Pool	6.9	Adrenal Gland	5.0
Fetal Kidney	3.1	Pituitary gland Pool	1.5
Renal ca. 786-0	9.0	Salivary Gland	2.3
Renal ca. A498	7.6	Thyroid (female)	2.0
Renal ca. ACHN	6.0	Pancreatic ca. CAPAN2	6.5
Renal ca. UO-31	6.3	Pancreas Pool	3.2

CNS_neurodegeneration_v1.0 Summary: Ag5265 This panel confirms the expression of the CG56870-04 gene at low levels in the brain in an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. Please see Panel 1.5 for a discussion of the potential utility of this gene in treatment of central nervous system disorders.

General_screening_panel_v1.5 Summary: Ag5265 Highest expression of the CG56870-05 gene is detected in cerebral cortex (CT=28.86). Thus, expression of this gene can be used in distinguishing this sample from other samples in the panel. Furthermore, significant expression of this gene is observed throughout the CNS, including in amygdala, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord. The CG56870-05 gene encodes a putative Ndr3 protein. This family consists of proteins from different gene families: Ndr1/RTP/Drg1/NDRG1, Ndr2, and Ndr3 (PFAM: IPR004142). NDRG1 is a cytoplasmic protein involved in stress responses, hormone responses, cell growth, and differentiation. Mutation of this gene was reported to be causative for hereditary motor and sensory neuropathy-Lom. Recently, NDRG4, another member of Ndr family, was shown to be expressed in neurons of the brain and spinal cord. Its expression was markedly decreased in the brain of Alzheimer's disease patient (Zhou et al., 2001). Therefore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

Among metabolic tissues, this gene has low levels of expression in heart, skeletal muscle, adrenal, thyroid, pancreas and pituitary. Therefore, this gene product may be important for the pathogenesis, diagnosis, and/or treatment of metabolic and endocrine disease, including Types 1 and 2 diabetes and obesity.

Overall, this gene is expressed in all the samples on this panel, with slightly higher levels of expression in the cancer cell lines compared to expression in the normal tissues samples.

Panel 4.1D Summary: Ag5265 Expression of this gene is low/undetectable (CTs > 34.5) across all of the samples on this panel (data not shown).

CF. CG59764-01: FERRITIN HEAVY CHAIN like protein

Expression of gene CG59764-01 was assessed using the primer-probe set Ag3578, described in Table CFA. Results of the RTQ-PCR runs are shown in Tables CFB and CFC.

Table CFA. Probe Name Ag3578

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-ctgcgacttcctggagaac-3'	19	430	659
Probe	TET-5'-agcaggccaagaccatcaaagagct-3'- TAMRA	25	462	660
Reverse	5'-tgtgcaggttgctcaggta-3'	19	494	661

Table CFB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3578, Run 210642348	Tissue Name	Rel. Exp.(%) Ag3578, Run 210642348
AD 1 Hippo	14.0	Control (Path) 3 Temporal Ctx	3.2
AD 2 Hippo	8.2	Control (Path) 4 Temporal Ctx	52.9
AD 3 Hippo	6.7	AD 1 Occipital Ctx	22.8
AD 4 Hippo	2.3	AD 2 Occipital Ctx (Missing)	0.0
AD 5 Hippo	83.5	AD 3 Occipital Ctx	7.3
AD 6 Hippo	29.1	AD 4 Occipital Ctx	14.9
Control 2 Hippo	1.6	AD 5 Occipital Ctx	11.4
Control 4 Hippo	3.1	AD 6 Occipital Ctx	19.8
Control (Path) 3 Hippo	8.0	Control 1 Occipital Ctx	9.0
AD 1 Temporal Ctx	19.5	Control 2 Occipital Ctx	29.5
AD 2 Temporal Ctx	22.8	Control 3 Occipital Ctx	24.0
AD 3 Temporal Ctx	17.0	Control 4 Occipital Ctx	7.4
AD 4 Temporal Ctx	16.8	Control (Path) 1 Occipital Ctx	38.4
AD 5 Inf Temporal Ctx	50.3	Control (Path) 2 Occipital Ctx	10.3
AD 5 Sup Temporal Ctx	40.6	Control (Path) 3 Occipital Ctx	0.0
AD 6 Inf Temporal Ctx	63.7	Control (Path) 4 Occipital Ctx	46.0
AD 6 Sup Temporal	100.0	Control 1 Parietal	9.2

Ctx		Ctx	
Control 1 Temporal Ctx	9.2	Control 2 Parietal Ctx	44.1
Control 2 Temporal Ctx	13.3	Control 3 Parietal Ctx	21.0
Control 3 Temporal Ctx	21.3	Control (Path) 1 Parietal Ctx	20.2
Control 3 Temporal Ctx	14.2	Control (Path) 2 Parietal Ctx	16.7
Control (Path) 1 Temporal Ctx	35.1	Control (Path) 3 Parietal Ctx	0.0
Control (Path) 2 Temporal Ctx	25.3	Control (Path) 4 Parietal Ctx	45.4

Table CFC. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3578, Run 217423081	Tissue Name	Rel. Exp.(%) Ag3578, Run 217423081
Adipose	8.6	Renal ca. TK-10	19.9
Melanoma* Hs688(A).T	0.0	Bladder	0.0
Melanoma* Hs688(B).T	0.0	Gastric ca. (liver met.) NCI-N87	15.3
Melanoma* M14	0.0	Gastric ca. KATO III	16.4
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	22.8
Melanoma* SK-MEL-5	0.0	Colon ca. SW480	5.6
Squamous cell carcinoma SCC-4	8.3	Colon ca.* (SW480 met) SW620	42.0
Testis Pool	27.4	Colon ca. HT29	2.6
Prostate ca.* (bone met) PC-3	11.0	Colon ca. HCT-116	39.2
Prostate Pool	0.0	Colon ca. CaCo-2	13.5
Placenta	15.3	Colon cancer tissue	4.8
Uterus Pool	0.0	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	0.0	Colon ca. Colo-205	4.2
Ovarian ca. SK-OV-3	14.4	Colon ca. SW-48	9.3
Ovarian ca. OVCAR-4	8.8	Colon Pool	27.5
Ovarian ca. OVCAR-5	16.6	Small Intestine Pool	11.2
Ovarian ca. IGROV-	13.0	Stomach Pool	11.3

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Ovarian ca. OVCAR-8	4.3	Bone Marrow Pool	8.7
Ovary	0.0	Fetal Heart	17.7
Breast ca. MCF-7	0.0	Heart Pool	9.9
Breast ca. MDA- MB-231	5.7	Lymph Node Pool	22.4
Breast ca. BT 549	47.3	Fetal Skeletal Muscle	10.2
Breast ca. T47D	8.0	Skeletal Muscle Pool	100.0
Breast ca. MDA-N	0.0	Spleen Pool	0.0
Breast Pool	7.6	Thymus Pool	3.5
Trachea	0.0	CNS cancer (glio/astro) U87-MG	0.0
Lung	3.1	CNS cancer (glio/astro) U-118-MG	8.1
Fetal Lung	7.1	CNS cancer (neuro;met) SK-N-AS	22.4
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF- 539	8.2
Lung ca. LX-1	49.7	CNS cancer (astro) SNB-75	25.2
Lung ca. NCI-H146	0.0	CNS cancer (glio) SNB-19	10.1
Lung ca. SHP-77	0.0	CNS cancer (glio) SF- 295	24.5
Lung ca. A549	0.0	Brain (Amygdala) Pool	7.8
Lung ca. NCI-H526	0.0	Brain (cerebellum)	20.3
Lung ca. NCI-H23	11.9	Brain (fetal)	18.7
Lung ca. NCI-H460	2.7	Brain (Hippocampus) Pool	14.9
Lung ca. HOP-62	10.9	Cerebral Cortex Pool	26.2
Lung ca. NCI-H522	0.0	Brain (Substantia nigra) Pool	35.4
Liver	0.0	Brain (Thalamus) Pool	19.1
Fetal Liver	0.0	Brain (whole)	17.3
Liver ca. HepG2	3.2	Spinal Cord Pool	9.2
Kidney Pool	21.5	Adrenal Gland	3.7
Fetal Kidney	21.2	Pituitary gland Pool	0.0
Renal ca. 786-0	11.7	Salivary Gland	0.0
Renal ca. A498	9.2	Thyroid (female)	6.7
Renal ca. ACHN	11.5	Pancreatic ca. CAPAN2	48.3
Renal ca. UO-31	10.3	Pancreas Pool	5.5

CNS_neurodegeneration_v1.0 Summary: Ag3578 This panel confirms the expression of the CG59764-01 gene at low levels in the brain in an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. Please see Panel 1.4 for a discussion of the potential utility of this gene in treatment of central nervous system disorders.

General_screening_panel_v1.4 Summary: Ag3578 Highest expression of the CG59764-01 gene is detected in sample derived from skeletal muscle (CT=31.2). Thus expression of this gene can be used to distinguish skeletal muscle sample from other samples used in this panel. This gene is also expressed at low but significant levels in heart and adipose. Thus, this gene product may be useful in the treatment of metabolic disorders that involve these tissues, including obesity.

Significant expression of this gene is also associated with samples derived from breast cancer, pancreatic cancer, colon cancer and lung cancer cell lines. Therefore, therapeutic modulation of the activity of this gene or its protein product might be beneficial in the treatment of these cancers.

In addition, this gene is expressed at low levels throughout the CNS, including in amygdala, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord. The CG59764-01 gene encodes a homologue of ferritin heavy chain protein (H-ferritin). It has been hypothesized that the up-regulation of the H-ferritin mRNA is part of a mechanism protecting the hippocampus, a seizure-prone area, against a possible overactivation during absence seizures (Lakaye et al., 2000). Therefore, therapeutic modulation of the expression or function of this gene may be useful in the treatment of seizure disorders, such as epilepsy. Furthermore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, multiple sclerosis, schizophrenia and depression.

References:

1. Lakaye B, de Borman B, Minet A, Arckens L, Vergnes M, Marescaux C, Grisar T. (2000) Increased expression of mRNA encoding ferritin heavy chain in brain structures of a rat model of absence epilepsy. *Exp Neurol* 162(1):112-20.

Panel 4.1D Summary: Ag3578 Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

CG. CG59710-01: P14

Expression of gene CG59710-01 was assessed using the primer-probe set Ag3512, described in Table CGA. Results of the RTQ-PCR runs are shown in Tables CGB and CGC.

Table CGA. Probe Name Ag3512

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-ctttgttctccagcacatctg-3'	21	211	662
Probe	TET-5'-ctacatcatggccgagatctgcaatg-3'- TAMRA	26	232	663
Reverse	5'-cctcgcatgtttaggatctg-3'	20	290	664

Table CGB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3512, Run 211004862	Tissue Name	Rel. Exp.(%) Ag3512, Run 211004862
AD 1 Hippo	23.0	Control (Path) 3 Temporal Ctx	7.2
AD 2 Hippo	31.2	Control (Path) 4 Temporal Ctx	37.1
AD 3 Hippo	9.8	AD 1 Occipital Ctx	20.0
AD 4 Hippo	10.0	AD 2 Occipital Ctx (Missing)	0.0
AD 5 hippo	85.9	AD 3 Occipital Ctx	9.0
AD 6 Hippo	56.6	AD 4 Occipital Ctx	21.3
Control 2 Hippo	41.5	AD 5 Occipital Ctx	15.2
Control 4 Hippo	21.6	AD 6 Occipital Ctx	49.0
Control (Path) 3 Hippo	12.5	Control 1 Occipital Ctx	6.0
AD 1 Temporal Ctx	31.9	Control 2 Occipital Ctx	77.4
AD 2 Temporal Ctx	41.2	Control 3 Occipital Ctx	22.1
AD 3 Temporal Ctx	11.3	Control 4 Occipital Ctx	9.8
AD 4 Temporal Ctx	21.0	Control (Path) 1 Occipital Ctx	77.9
AD 5 Inf Temporal Ctx	100.0	Control (Path) 2 Occipital Ctx	12.6

AD 5 SupTemporal Ctx	42.6	Control (Path) 3 Occipital Ctx	5.4
AD 6 Inf Temporal Ctx	35.1	Control (Path) 4 Occipital Ctx	21.6
AD 6 Sup Temporal Ctx	56.6	Control 1 Parietal Ctx	11.4
Control 1 Temporal Ctx	10.1	Control 2 Parietal Ctx	52.5
Control 2 Temporal Ctx	53.2	Control 3 Parietal Ctx	21.5
Control 3 Temporal Ctx	17.2	Control (Path) 1 Parietal Ctx	68.8
Control 4 Temporal Ctx	15.9	Control (Path) 2 Parietal Ctx	29.7
Control (Path) 1 Temporal Ctx	55.1	Control (Path) 3 Parietal Ctx	10.2
Control (Path) 2 Temporal Ctx	39.5	Control (Path) 4 Parietal Ctx	48.3

Table CGC. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3512, Run 217240776	Tissue Name	Rel. Exp.(%) Ag3512, Run 217240776
Adipose	3.3	Renal ca. TK-10	21.8
Melanoma* Hs688(A).T	9.7	Bladder	5.5
Melanoma* Hs688(B).T	10.5	Gastric ca. (liver met.) NCI-N87	37.1
Melanoma* M14	26.4	Gastric ca. KATO III	48.6
Melanoma* LOXIMVI	35.4	Colon ca. SW-948	7.2
Melanoma* SK-MEL-5	14.4	Colon ca. SW480	62.4
Squamous cell carcinoma SCC-4	14.9	Colon ca.* (SW480 met) SW620	29.7
Testis Pool	6.7	Colon ca. HT29	14.6
Prostate ca.* (bone met) PC-3	17.2	Colon ca. HCT-116	24.1
Prostate Pool	4.8	Colon ca. CaCo-2	46.0
Placenta	4.4	Colon cancer tissue	13.9
Uterus Pool	3.1	Colon ca. SW1116	2.1
Ovarian ca. OVCAR-3	20.0	Colon ca. Colo-205	10.8
Ovarian ca. SK-OV-3	31.6	Colon ca. SW-48	11.9

Ovarian ca. OVCAR-4	19.6	Colon Pool	13.4
Ovarian ca. OVCAR-5	30.8	Small Intestine Pool	7.0
Ovarian ca. IGROV-1	10.2	Stomach Pool	4.0
Ovarian ca. OVCAR-8	14.0	Bone Marrow Pool	2.4
Ovary	3.6	Fetal Heart	3.3
Breast ca. MCF-7	18.2	Heart Pool	4.1
Breast ca. MDA-MB-231	33.7	Lymph Node Pool	7.5
Breast ca. BT 549	24.8	Fetal Skeletal Muscle	1.8
Breast ca. T47D	100.0	Skeletal Muscle Pool	6.3
Breast ca. MDA-N	24.8	Spleen Pool	10.8
Breast Pool	7.3	Thymus Pool	5.9
Trachea	2.8	CNS cancer (glio/astro) U87-MG	33.7
Lung	3.1	CNS cancer (glio/astro) U-118-MG	30.1
Fetal Lung	7.0	CNS cancer (neuro;met) SK-N-AS	13.3
Lung ca. NCI-N417	7.3	CNS cancer (astro) SF-539	16.2
Lung ca. LX-1	17.6	CNS cancer (astro) SNB-75	46.3
Lung ca. NCI-H146	13.1	CNS cancer (glio) SNB-19	10.6
Lung ca. SHP-77	21.0	CNS cancer (glio) SF-295	27.5
Lung ca. A549	25.7	Brain (Amygdala) Pool	4.1
Lung ca. NCI-H526	15.0	Brain (cerebellum)	6.7
Lung ca. NCI-H23	30.8	Brain (fetal)	6.7
Lung ca. NCI-H460	9.3	Brain (Hippocampus) Pool	4.4
Lung ca. HOP-62	6.7	Cerebral Cortex Pool	6.3
Lung ca. NCI-H522	15.2	Brain (Substantia nigra) Pool	6.1
Liver	1.3	Brain (Thalamus) Pool	5.6
Fetal Liver	7.7	Brain (whole)	4.7
Liver ca. HepG2	11.2	Spinal Cord Pool	4.5
Kidney Pool	12.9	Adrenal Gland	3.3
Fetal Kidney	4.2	Pituitary gland Pool	2.6
Renal ca. 786-0	11.8	Salivary Gland	2.5

Renal ca. A498	6.1	Thyroid (female)	3.5
Renal ca. ACHN	10.5	Pancreatic ca. CAPAN2	15.3
Renal ca. UO-31	18.2	Pancreas Pool	7.6

CNS_neurodegeneration_v1.0 Summary: Ag3512 This panel confirms the expression of the CG59710-01 gene at low levels in the brain in an independent group of individuals.

However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. However, as seen in panel 1.4, this gene is expressed at low levels throughout the CNS, including in amygdala, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord. Therefore, this gene may play a role in other central nervous system disorders such as Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

General_screening_panel_v1.4 Summary: Ag3512 Highest expression of the CG59710-01 gene is detected in a sample derived from a breast cancer cell line (CT=25.3). Therefore, expression of this gene could be used in distinguishing this sample from other samples in the panel. Overall, expression of this gene appears to be associated with the cancer cell lines suggesting a role for this gene product in cellular growth and proliferation. Specifically, significant expression of this gene is associated with CNS cancer, colon cancer, gastric cancer, renal cancer, lung cancer, breast cancer, ovarian cancer, and melanoma cancer cell lines. Therefore, therapeutic modulation of the activity of this gene or its protein product might be beneficial in the treatment of these cancers.

Panel 4.1D Summary: Ag3512 Results from one experiment with the CG59710-01 gene are not included. The amp plot indicates that there were experimental difficulties with this run.

CH. CG59754-02 and CG59754-01: DOWN SYNDROME CELL ADHESION MOLECULE

Expression of gene CG59754-02 and variant CG59754-01 was assessed using the primer-probe set Ag1305, described in Table CHA.

Table CHA. Probe Name Ag1305

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-gtgagcattgtgtctccagaa-3'	21	291	665
Probe	TET-5'-tttattacctaccacggcggctgta-3'-	26	321	666

	TAMRA			
Reverse	5' -tcctccttctgtacgtcagaga-3'	22	349	667

Panel 4D Summary: Ag1305 Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

CI. CG59800-01: HEPARAN SULFATE D-GLUCOSAMINYL 3-O-SULFOTRANSFERASE-3B

Expression of gene CG59800-01 was assessed using the primer-probe set Ag3589, described in Table CIA.

Table CIA. Probe Name Ag3589

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5' -tacatacctgcccgtgccatac-3'	22	88	668
Probe	TET-5' -ctacatacctgccccgtccatacctg-3' - TAMRA	26	117	669
Reverse	5' -gtatggacggggcaggtat-3'	19	121	670

Results from Panels CNS_neurodegeneration_v1.0, 1.4, 2.2, and 4.1D are not included. The amp plots corresponding to these runs suggest that there were experimental difficulties with these runs.

CJ. CG59761-01: AXIN 1 (AXIS INHIBITION PROTEIN 1) (HAXIN) - isoform1, submitted to study DDSMT on 03/21/01 by cmiller; clone status=FIS; novelty=Novel; ORF start=97, ORF stop=2833, frame=1; 2949 bp.

Expression of gene CG59761-01 was assessed using the primer-probe set Ag3577, described in Table CJA. Results of the RTQ-PCR runs are shown in Tables CJB, CJC and CJD.

Table CJA. Probe Name Ag3577

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5' -atacttgaagtgggctgagtc-3'	22	486	671
Probe	TET-5' -cattccctgctggatgaccaagatg-3' - TAMRA	25	511	672
Reverse	5' -aggaaagtctctgaacaggctta-3'	22	539	673

Table CJB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3577, Run 210642177	Tissue Name	Rel. Exp.(%) Ag3577, Run 210642177
AD 1 Hippo	26.1	Control (Path) 3 Temporal Ctx	7.5
AD 2 Hippo	20.6	Control (Path) 4 Temporal Ctx	26.8
AD 3 Hippo	10.8	AD 1 Occipital Ctx	23.5
AD 4 Hippo	9.1	AD 2 Occipital Ctx (Missing)	0.0
AD 5 hippo	86.5	AD 3 Occipital Ctx	12.3
AD 6 Hippo	48.3	AD 4 Occipital Ctx	18.9
Control 2 Hippo	21.8	AD 5 Occipital Ctx	24.3
Control 4 Hippo	16.6	AD 6 Occipital Ctx	34.4
Control (Path) 3 Hippo	4.7	Control 1 Occipital Ctx	6.2
AD 1 Temporal Ctx	25.7	Control 2 Occipital Ctx	57.4
AD 2 Temporal Ctx	28.3	Control 3 Occipital Ctx	13.4
AD 3 Temporal Ctx	14.5	Control 4 Occipital Ctx	8.7
AD 4 Temporal Ctx	19.8	Control (Path) 1 Occipital Ctx	62.4
AD 5 Inf Temporal Ctx	100.0	Control (Path) 2 Occipital Ctx	10.5
AD 5 Sup Temporal Ctx	44.1	Control (Path) 3 Occipital Ctx	5.3
AD 6 Inf Temporal Ctx	48.3	Control (Path) 4 Occipital Ctx	20.4
AD 6 Sup Temporal Ctx	47.0	Control 1 Parietal Ctx	15.9
Control 1 Temporal Ctx	11.6	Control 2 Parietal Ctx	54.3
Control 2 Temporal Ctx	35.1	Control 3 Parietal Ctx	15.5
Control 3 Temporal Ctx	14.6	Control (Path) 1 Parietal Ctx	43.5
Control 4 Temporal Ctx	12.9	Control (Path) 2 Parietal Ctx	21.3
Control (Path) 1 Temporal Ctx	47.0	Control (Path) 3 Parietal Ctx	7.0
Control (Path) 2 Temporal Ctx	28.5	Control (Path) 4 Parietal Ctx	39.0

Table CJC. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3577, Run 217343282	Tissue Name	Rel. Exp.(%) Ag3577, Run 217343282
Adipose	2.8	Renal ca. TK-10	35.4
Melanoma* Hs688(A).T	13.9	Bladder	13.3
Melanoma* Hs688(B).T	13.7	Gastric ca. (liver met.) NCI-N87	70.7
Melanoma* M14	28.5	Gastric ca. KATO III	100.0
Melanoma* LOXIMVI	21.2	Colon ca. SW-948	15.0
Melanoma* SK- MEL-5	24.3	Colon ca. SW480	43.5
Squamous cell carcinoma SCC-4	23.2	Colon ca. * (SW480 met) SW620	47.6
Testis Pool	6.4	Colon ca. HT29	26.2
Prostate ca.* (bone met) PC-3	32.3	Colon ca. HCT-116	27.2
Prostate Pool	5.1	Colon ca. CaCo-2	35.4
Placenta	6.2	Colon cancer tissue	13.1
Uterus Pool	2.8	Colon ca. SW1116	14.2
Ovarian ca. OVCAR-3	12.5	Colon ca. Colo-205	10.1
Ovarian ca. SK-OV- 3	56.6	Colon ca. SW-48	21.8
Ovarian ca. OVCAR-4	11.4	Colon Pool	10.7
Ovarian ca. OVCAR-5	42.0	Small Intestine Pool	10.4
Ovarian ca. IGROV- 1	12.9	Stomach Pool	5.6
Ovarian ca. OVCAR-8	13.1	Bone Marrow Pool	5.2
Ovary	7.3	Fetal Heart	3.5
Breast ca. MCF-7	29.3	Heart Pool	4.0
Breast ca. MDA- MB-231	32.3	Lymph Node Pool	12.7
Breast ca. BT 549	30.1	Fetal Skeletal Muscle	3.6
Breast ca. T47D	75.3	Skeletal Muscle Pool	10.6
Breast ca. MDA-N	21.8	Spleen Pool	7.3
Breast Pool	12.3	Thymus Pool	13.9
Trachea	10.8	CNS cancer (glio/astro) U87-MG	10.7
Lung	1.8	CNS cancer (glio/astro) U-118-MG	42.9

Fetal Lung	16.0	CNS cancer (neuro;met) SK-N-AS	25.3
Lung ca. NCI-N417	7.0	CNS cancer (astro) SF-539	6.0
Lung ca. LX-1	79.0	CNS cancer (astro) SNB-75	34.2
Lung ca. NCI-H146	12.3	CNS cancer (glio) SNB-19	13.8
Lung ca. SHP-77	29.1	CNS cancer (glio) SF-295	28.1
Lung ca. A549	29.1	Brain (Amygdala) Pool	5.3
Lung ca. NCI-H526	7.4	Brain (cerebellum)	34.9
Lung ca. NCI-H23	28.3	Brain (fetal)	21.5
Lung ca. NCI-H460	23.3	Brain (Hippocampus) Pool	5.4
Lung ca. HOP-62	7.8	Cerebral Cortex Pool	6.3
Lung ca. NCI-H522	28.5	Brain (Substantia nigra) Pool	6.6
Liver	0.9	Brain (Thalamus) Pool	8.1
Fetal Liver	12.5	Brain (whole)	11.6
Liver ca. HepG2	26.8	Spinal Cord Pool	5.1
Kidney Pool	14.1	Adrenal Gland	10.1
Fetal Kidney	7.2	Pituitary gland Pool	0.0
Renal ca. 786-0	13.6	Salivary Gland	5.9
Renal ca. A498	7.9	Thyroid (female)	5.3
Renal ca. ACHN	22.1	Pancreatic ca. CAPAN2	30.8
Renal ca. UO-31	17.7	Pancreas Pool	13.9

Table CJD. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag3577, Run 169851850	Tissue Name	Rel. Exp.(%) Ag3577, Run 169851850
Secondary Th1 act	50.0	HUVEC IL-1beta	37.9
Secondary Th2 act	57.0	HUVEC IFN gamma	25.5
Secondary Tr1 act	71.2	HUVEC TNF alpha + IFN gamma	35.8
Secondary Th1 rest	29.5	HUVEC TNF alpha + IL4	36.9
Secondary Th2 rest	58.2	HUVEC IL-11	14.6
Secondary Tr1 rest	55.1	Lung Microvascular EC none	48.0
Primary Th1 act	62.9	Lung Microvascular EC TNFalpha + IL-1beta	45.7
Primary Th2 act	61.6	Microvascular Dermal EC	27.5

		none	
Primary Tr1 act	60.7	Microsvascular Dermal EC TNFalpha + IL-1beta	24.1
Primary Th1 rest	50.3	Bronchial epithelium TNFalpha + IL1beta	39.2
Primary Th2 rest	61.1	Small airway epithelium none	20.4
Primary Tr1 rest	85.3	Small airway epithelium TNFalpha + IL-1beta	57.8
CD45RA CD4 lymphocyte act	47.6	Coronary artery SMC rest	13.9
CD45RO CD4 lymphocyte act	58.6	Coronary artery SMC TNFalpha + IL-1beta	12.9
CD8 lymphocyte act	55.5	Astrocytes rest	16.8
Secondary CD8 lymphocyte rest	51.4	Astrocytes TNFalpha + IL-1beta	18.7
Secondary CD8 lymphocyte act	31.0	KU-812 (Basophil) rest	37.1
CD4 lymphocyte none	33.2	KU-812 (Basophil) PMA/ionomycin	64.2
2ry Th1/Th2/Tr1 _anti- CD95 CH11	54.3	CCD1106 (Keratinocytes) none	48.0
LAK cells rest	52.1	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	43.8
LAK cells IL-2	50.3	Liver cirrhosis	7.5
LAK cells IL-2+IL-12	47.0	NCI-H292 none	30.6
LAK cells IL-2+IFN gamma	62.9	NCI-H292 IL-4	60.3
LAK cells IL-2+ IL-18	61.1	NCI-H292 IL-9	72.2
LAK cells PMA/ionomycin	95.9	NCI-H292 IL-13	57.8
NK Cells IL-2 rest	100.0	NCI-H292 IFN gamma	85.9
Two Way MLR 3 day	74.7	HPAEC none	23.0
Two Way MLR 5 day	50.7	HPAEC TNF alpha + IL-1 beta	33.4
Two Way MLR 7 day	27.9	Lung fibroblast none	15.3
PBMC rest	58.2	Lung fibroblast TNF alpha + IL-1 beta	17.4
PBMC PWM	46.7	Lung fibroblast IL-4	23.7
PBMC PHA-L	29.9	Lung fibroblast IL-9	29.3
Ramos (B cell) none	39.2	Lung fibroblast IL-13	30.4
Ramos (B cell) ionomycin	42.6	Lung fibroblast IFN gamma	36.3
B lymphocytes PWM	31.9	Dermal fibroblast CCD1070 rest	47.3

B lymphocytes CD40L and IL-4	49.7	Dermal fibroblast CCD1070 TNF alpha	94.6
EOL-1 dbcAMP	59.5	Dermal fibroblast CCD1070 IL-1 beta	20.6
EOL-1 dbcAMP PMA/ionomycin	55.1	Dermal fibroblast IFN gamma	25.0
Dendritic cells none	47.6	Dermal fibroblast IL-4	34.6
Dendritic cells LPS	41.2	Dermal Fibroblasts rest	22.4
Dendritic cells anti-CD40	62.4	Neutrophils TNFa+LPS	10.2
Monocytes rest	50.3	Neutrophils rest	28.9
Monocytes LPS	63.7	Colon	20.2
Macrophages rest	46.0	Lung	21.9
Macrophages LPS	27.7	Thymus	57.0
HUVEC none	15.8	Kidney	15.8
HUVEC starved	29.9		

CNS_neurodegeneration_v1.0 Summary: Ag3577 This panel confirms the expression of the CG59671-01 gene at low levels in the brain in an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. As seen in panel 1.4, this gene is expressed at low levels throughout the CNS, including in amygdala, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord. Therefore, this gene may play a role in other central nervous system disorders such as Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

General_screening_panel_v1.4 Summary: Ag3577 Highest expression of the CG59671-01 gene is detected in a gastric cancer cell line sample (CTs=27.3). In addition, significant expression of this gene is associated with clusters of cell lines derived from ovarian cancer, breast cancer, and gastric cancer. Therefore, expression of this gene might be used to differentiate between these samples and other samples on this panel and as a marker for these cancers. The CG59671-01 gene encodes an Axin 1 protein, which is known play an important role in Wnt signalling transduction pathway. The Wnt/Wingless signaling transduction pathway plays an important role in both embryonic development and tumorigenesis. Beta-Catenin, a key component of the Wnt signaling pathway, interacts with the TCF/LEF family of transcription factors and activates transcription of Wnt target genes. A number of proteins such as the tumor suppressor APC and Axin are also involved in the regulation of the Wnt signaling pathway. Furthermore, mutations in APC or beta-catenin have been found to be

responsible for the genesis of human cancers (Akiyama T, 2000). Recently, Dahmen et al. (2001) have shown presence of a single somatic point mutation in exon 1 (Pro255Ser) and deletion of seven large of AXIN1 (12%) in 86 medulloblastoma (MB) samples and 11 MB cell lines. Therefore, AXIN1 may play a role as tumor suppressor gene in MBs. Furthermore, therapeutic modulation of the activity of this gene or its protein product might be beneficial in the treatment of these cancers.

Among tissues with metabolic function, this gene is expressed at moderate to low levels in pituitary, adipose, adrenal gland, pancreas, thyroid, and adult and fetal skeletal muscle, heart, and liver. This widespread expression among these tissues suggests that this gene product may play a role in normal neuroendocrine and metabolic and that dysregulated expression of this gene may contribute to neuroendocrine disorders or metabolic diseases, such as obesity and diabetes.

This gene is also expressed in all regions of the CNS examined. Please see Panel CNS_neurodegeneration_v1.0 for discussion of utility of this gene in the central nervous system.

References:

1. Akiyama T. (2000) Wnt/beta-catenin signaling. Cytokine Growth Factor Rev 11(4):273-82.
2. Dahmen RP, Koch A, Denkhaus D, Tonn JC, Sorensen N, Berthold F, Behrens J, Birchmeier W, Wiestler OD, Pietsch T. (2001) Deletions of AXIN1, a component of the WNT/wingless pathway, in sporadic medulloblastomas. Cancer Res 2001 Oct 1;61(19):7039-43

Panel 4.1D Summary: Ag3577 Highest expression of the CG59671-01 gene is detected in resting NK Cells IL-2 cells (CTs=28.3). In addition, this gene is expressed at high to moderate levels in a wide range of cell types of significance in the immune response in health and disease. These cells include members of the T-cell, B-cell, endothelial cell, macrophage/monocyte, and peripheral blood mononuclear cell family, as well as epithelial and fibroblast cell types from lung and skin, and normal tissues represented by colon, lung, thymus and kidney. This ubiquitous pattern of expression suggests that this gene product may be involved in homeostatic processes for these and other cell types and tissues. Therefore,

modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

CK. CG59708-01 and CG59708-02 and CG59708-03: Ubiquitin carboxyl-terminal hydrolase 21

Expression of gene CG59708-01, full length clone CG59708-03 and variant CG59708-02 was assessed using the primer-probe set Ag3511, described in Table CKA. Results of the RTQ-PCR runs are shown in Tables CKB, CKC and CKD. Please note that CG59708-03 represents a full-length physical clone of the CG59708-01 gene, validating the prediction of the gene sequence.

Table CKA. Probe Name Ag3511

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-acccaaaagggtagtagaacga-3'	22	2431	674
Probe	TET-5'-cccttctggaacagtttgcagataaa-3'- TAMRA	26	2454	675
Reverse	5'-gccaccttcataatgctgatt-3'	21	2503	676

Table CKB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3511, Run 210499621	Tissue Name	Rel. Exp.(%) Ag3511, Run 210499621
AD 1 Hippo	8.2	Control (Path) 3 Temporal Ctx	4.1
AD 2 Hippo	17.9	Control (Path) 4 Temporal Ctx	32.1
AD 3 Hippo	6.0	AD 1 Occipital Ctx	17.7
AD 4 Hippo	4.1	AD 2 Occipital Ctx (Missing)	0.0
AD 5 Hippo	87.1	AD 3 Occipital Ctx	3.1
AD 6 Hippo	52.5	AD 4 Occipital Ctx	20.0
Control 2 Hippo	13.0	AD 5 Occipital Ctx	22.4
Control 4 Hippo	6.4	AD 6 Occipital Ctx	21.6
Control (Path) 3 Hippo	3.4	Control 1 Occipital Ctx	2.5
AD 1 Temporal Ctx	15.0	Control 2 Occipital	39.5

		Ctx	
AD 2 Temporal Ctx	22.7	Control 3 Occipital Ctx	18.6
AD 3 Temporal Ctx	4.5	Control 4 Occipital Ctx	3.8
AD 4 Temporal Ctx	20.0	Control (Path) 1 Occipital Ctx	61.6
AD 5 Inf Temporal Ctx	100.0	Control (Path) 2 Occipital Ctx	10.4
AD 5 Sup Temporal Ctx	36.6	Control (Path) 3 Occipital Ctx	2.4
AD 6 Inf Temporal Ctx	46.7	Control (Path) 4 Occipital Ctx	14.1
AD 6 Sup Temporal Ctx	58.6	Control 1 Parietal Ctx	5.3
Control 1 Temporal Ctx	5.6	Control 2 Parietal Ctx	47.0
Control 2 Temporal Ctx	20.2	Control 3 Parietal Ctx	14.7
Control 3 Temporal Ctx	15.8	Control (Path) 1 Parietal Ctx	57.4
Control 3 Temporal Ctx	6.1	Control (Path) 2 Parietal Ctx	27.4
Control (Path) 1 Temporal Ctx	50.0	Control (Path) 3 Parietal Ctx	2.2
Control (Path) 2 Temporal Ctx	33.2	Control (Path) 4 Parietal Ctx	37.1

Table CKC. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3511, Run 217240774	Tissue Name	Rel. Exp.(%) Ag3511, Run 217240774
Adipose	4.9	Renal ca. TK-10	18.4
Melanoma* Hs688(A).T	15.9	Bladder	9.3
Melanoma* Hs688(B).T	12.8	Gastric ca. (liver met.) NCI-N87	24.3
Melanoma* M14	20.6	Gastric ca. KATO III	100.0
Melanoma* LOXIMVI	9.1	Colon ca. SW-948	4.7
Melanoma* SK-MEL-5	26.6	Colon ca. SW480	63.7
Squamous cell carcinoma SCC-4	14.3	Colon ca.* (SW480 met) SW620	26.1
Testis Pool	6.3	Colon ca. HT29	17.4

Prostate ca. * (bone met) PC-3	43.5	Colon ca. HCT-116	24.3
Prostate Pool	6.6	Colon ca. CaCo-2	54.7
Placenta	0.7	Colon cancer tissue	6.5
Uterus Pool	4.4	Colon ca. SW1116	4.8
Ovarian ca. OVCAR-3	11.7	Colon ca. Colo-205	2.0
Ovarian ca. SK-OV-3	45.1	Colon ca. SW-48	4.0
Ovarian ca. OVCAR-4	17.9	Colon Pool	13.0
Ovarian ca. OVCAR-5	26.1	Small Intestine Pool	14.1
Ovarian ca. IGROV-1	12.5	Stomach Pool	7.2
Ovarian ca. OVCAR-8	10.2	Bone Marrow Pool	6.5
Ovary	7.5	Fetal Heart	73.2
Breast ca. MCF-7	9.7	Heart Pool	19.1
Breast ca. MDA-MB-231	47.0	Lymph Node Pool	14.5
Breast ca. BT 549	58.2	Fetal Skeletal Muscle	34.9
Breast ca. T47D	44.1	Skeletal Muscle Pool	45.1
Breast ca. MDA-N	12.9	Spleen Pool	9.8
Breast Pool	15.2	Thymus Pool	13.0
Trachea	7.1	CNS cancer (glio/astro) U87-MG	2.6
Lung	3.8	CNS cancer (glio/astro) U-118-MG	33.4
Fetal Lung	27.5	CNS cancer (neuro;met) SK-N-AS	8.5
Lung ca. NCI-N417	2.5	CNS cancer (astro) SF-539	11.6
Lung ca. LX-1	24.0	CNS cancer (astro) SNB-75	31.6
Lung ca. NCI-H146	3.2	CNS cancer (glio) SNB-19	12.1
Lung ca. SHP-77	13.0	CNS cancer (glio) SF-295	40.9
Lung ca. A549	18.9	Brain (Amygdala) Pool	4.7
Lung ca. NCI-H526	20.6	Brain (cerebellum)	12.0
Lung ca. NCI-H23	23.5	Brain (fetal)	10.7
Lung ca. NCI-H460	10.5	Brain (Hippocampus) Pool	3.8

Lung ca. HOP-62	10.2	Cerebral Cortex Pool	7.5
Lung ca. NCI-H522	21.8	Brain (Substantia nigra) Pool	3.2
Liver	1.6	Brain (Thalamus) Pool	8.0
Fetal Liver	10.9	Brain (whole)	5.0
Liver ca. HepG2	7.2	Spinal Cord Pool	3.8
Kidney Pool	16.3	Adrenal Gland	5.0
Fetal Kidney	16.3	Pituitary gland Pool	3.0
Renal ca. 786-0	11.3	Salivary Gland	3.1
Renal ca. A498	4.2	Thyroid (female)	3.1
Renal ca. ACHN	10.2	Pancreatic ca. CAPAN2	25.0
Renal ca. UO-31	17.1	Pancreas Pool	13.0

Table CKD. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3511, Run 166407112	Tissue Name	Rel. Exp.(%) Ag3511, Run 166407112
Secondary Th1 act	26.6	HUVEC IL-1beta	14.8
Secondary Th2 act	31.6	HUVEC IFN gamma	16.8
Secondary Tr1 act	33.7	HUVEC TNF alpha + IFN gamma	9.7
Secondary Th1 rest	22.8	HUVEC TNF alpha + IL4	9.1
Secondary Th2 rest	17.2	HUVEC IL-11	9.9
Secondary Tr1 rest	20.3	Lung Microvascular EC none	13.2
Primary Th1 act	10.4	Lung Microvascular EC TNFalpha + IL-1beta	8.3
Primary Th2 act	17.2	Microvascular Dermal EC none	22.7
Primary Tr1 act	25.7	Microvascular Dermal EC TNFalpha + IL-1beta	11.9
Primary Th1 rest	57.4	Bronchial epithelium TNFalpha + IL1beta	8.0
Primary Th2 rest	28.1	Small airway epithelium none	3.7
Primary Tr1 rest	15.6	Small airway epithelium TNFalpha + IL-1beta	24.3
CD45RA CD4 lymphocyte act	11.0	Coronary artery SMC rest	11.9
CD45RO CD4 lymphocyte act	28.1	Coronary artery SMC TNFalpha + IL-1beta	7.6
CD8 lymphocyte act	19.2	Astrocytes rest	10.6
Secondary CD8	15.3	Astrocytes TNFalpha +	12.4

lymphocyte rest		IL-1beta	
Secondary CD8 lymphocyte act	20.3	KU-812 (Basophil) rest	20.2
CD4 lymphocyte none	8.4	KU-812 (Basophil) PMA/ionomycin	46.7
2ry Th1/Th2/Tr1_anti-CD95 CH11	24.8	CCD1106 (Keratinocytes) none	12.6
LAK cells rest	12.2	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	53.2
LAK cells IL-2	49.3	Liver cirrhosis	7.7
LAK cells IL-2+IL-12	27.5	Lupus kidney	9.7
LAK cells IL-2+IFN gamma	47.6	NCI-H292 none	59.5
LAK cells IL-2+ IL-18	35.4	NCI-H292 IL-4	100.0
LAK cells PMA/ionomycin	3.6	NCI-H292 IL-9	69.7
NK Cells IL-2 rest	46.0	NCI-H292 IL-13	46.7
Two Way MLR 3 day	24.7	NCI-H292 IFN gamma	36.6
Two Way MLR 5 day	22.1	HPAEC none	11.8
Two Way MLR 7 day	13.9	HPAEC TNF alpha + IL-1 beta	12.9
PBMC rest	13.0	Lung fibroblast none	13.3
PBMC PWM	17.3	Lung fibroblast TNF alpha + IL-1 beta	31.9
PBMC PHA-L	11.7	Lung fibroblast IL-4	9.6
Ramos (B cell) none	19.8	Lung fibroblast IL-9	7.4
Ramos (B cell) ionomycin	18.2	Lung fibroblast IL-13	6.3
B lymphocytes PWM	37.1	Lung fibroblast IFN gamma	10.4
B lymphocytes CD40L and IL-4	34.6	Dermal fibroblast CCD1070 rest	23.7
EOL-1 dbcAMP	14.4	Dermal fibroblast CCD1070 TNF alpha	75.8
EOL-1 dbcAMP PMA/ionomycin	21.6	Dermal fibroblast CCD1070 IL-1 beta	18.7
Dendritic cells none	10.8	Dermal fibroblast IFN gamma	5.6
Dendritic cells LPS	13.5	Dermal fibroblast IL-4	11.3
Dendritic cells anti-CD40	14.4	IBD Colitis 2	5.3
Monocytes rest	11.6	IBD Crohn's	6.0
Monocytes LPS	7.6	Colon	52.9
Macrophages rest	20.3	Lung	9.7

Macrophages LPS	15.0	Thymus	16.3
HUVEC none	16.8	Kidney	19.9
HUVEC starved	29.9		

CNS_neurodegeneration_v1.0 Summary: Ag3511 This panel confirms the expression of CG59708-01 gene at low levels in the brain in an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. However, as seen in panel 1.4, this gene is expressed at low levels throughout the CNS, including in amygdala, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord. Therefore, this gene may play a role in other central nervous system disorders such as Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

General_screening_panel_v1.4 Summary: Ag3511 Highest expression of the CG59708-01 is detected in a gastric cancer cell line sample (CT=27.1). Thus, expression of this gene can be used to distinguish this sample from other samples in this panel. In addition, high levels of expression of this gene are associated with breast cancer, ovarian cancer, and gastric cancer cell lines. Therefore, therapeutic modulation of the activity of this gene or its protein product might be beneficial in the treatment of these cancers.

Among tissues with metabolic function, this gene is expressed at moderate to low levels in pituitary, adipose, adrenal gland, pancreas, thyroid, and adult and fetal skeletal muscle, heart, and liver. This widespread expression among these tissues suggests that this gene product may play a role in normal neuroendocrine and metabolic and that dysregulated expression of this gene may contribute to neuroendocrine disorders or metabolic diseases, such as obesity and diabetes.

This gene is also expressed at moderate to low levels in all regions of the CNS examined. Please see Panel CNS_neurodegeneration_v1.0 for discussion of utility of this gene in the central nervous system.

Panel 4D Summary: Ag3511 Highest expression of the CG59708-01 gene is detected in a IL-4 treated NCI-H292 sample (CT=26.4). In addition, this gene is expressed at high to moderate levels in a wide range of cell types of significance in the immune response in health and disease. These cells include members of the T-cell, B-cell, endothelial cell, macrophage/monocyte, and peripheral blood mononuclear cell family, as well as epithelial and

fibroblast cell types from lung and skin, and normal tissues represented by colon, lung, thymus and kidney. This ubiquitous pattern of expression suggests that this gene product may be involved in homeostatic processes for these and other cell types and tissues. This pattern is in agreement with the expression profile in General_screening_panel_v1.5 and also suggests a role for the gene product in cell survival and proliferation. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

CL. CG59559-01: CPSase-related

Expression of gene CG59559-01 was assessed using the primer-probe set Ag3469, described in Table CLA. Results of the RTQ-PCR runs are shown in Tables CLB, CLC and CLD.

Table CLA. Probe Name Ag3469

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-tccagtcggatcaattctattg-3'	22	1213	677
Probe	TET-5'-attcagatgtccctcatcagcccat-3'-TAMRA	26	1237	678
Reverse	5'-aattgtcttcgacgaagaaacc-3'	22	1266	679

Table CLB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3469, Run 210376662	Tissue Name	Rel. Exp.(%) Ag3469, Run 210376662
AD 1 Hippo	23.5	Control (Path) 3 Temporal Ctx	13.9
AD 2 Hippo	31.0	Control (Path) 4 Temporal Ctx	35.6
AD 3 Hippo	17.1	AD 1 Occipital Ctx	8.1
AD 4 Hippo	23.0	AD 2 Occipital Ctx (Missing)	0.0
AD 5 Hippo	21.0	AD 3 Occipital Ctx	2.0
AD 6 Hippo	69.3	AD 4 Occipital Ctx	25.9
Control 2 Hippo	56.6	AD 5 Occipital Ctx	31.9
Control 4 Hippo	52.5	AD 6 Occipital Ctx	10.4
Control (Path) 3	7.5	Control 1 Occipital	3.3

Hippo		Ctx	
AD 1 Temporal Ctx	39.8	Control 2 Occipital Ctx	42.6
AD 2 Temporal Ctx	35.8	Control 3 Occipital Ctx	10.7
AD 3 Temporal Ctx	12.2	Control 4 Occipital Ctx	17.6
AD 4 Temporal Ctx	30.1	Control (Path) 1 Occipital Ctx	59.0
AD 5 Inf Temporal Ctx	37.6	Control (Path) 2 Occipital Ctx	14.6
AD 5 Sup Temporal Ctx	33.4	Control (Path) 3 Occipital Ctx	0.0
AD 6 Inf Temporal Ctx	52.1	Control (Path) 4 Occipital Ctx	10.6
AD 6 Sup Temporal Ctx	31.0	Control 1 Parietal Ctx	9.1
Control 1 Temporal Ctx	12.7	Control 2 Parietal Ctx	28.5
Control 2 Temporal Ctx	31.4	Control 3 Parietal Ctx	17.2
Control 3 Temporal Ctx	36.3	Control (Path) 1 Parietal Ctx	64.2
Control 3 Temporal Ctx	16.8	Control (Path) 2 Parietal Ctx	25.7
Control (Path) 1 Temporal Ctx	100.0	Control (Path) 3 Parietal Ctx	1.3
Control (Path) 2 Temporal Ctx	62.4	Control (Path) 4 Parietal Ctx	55.9

Table CLC. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3469, Run 217119419	Tissue Name	Rel. Exp.(%) Ag3469, Run 217119419
Adipose	3.8	Renal ca. TK-10	7.1
Melanoma* Hs688(A).T	9.2	Bladder	5.7
Melanoma* Hs688(B).T	4.7	Gastric ca. (liver met.) NCI-N87	4.9
Melanoma* M14	0.1	Gastric ca. KATO III	1.0
Melanoma* LOXIMVI	0.8	Colon ca. SW-948	0.8
Melanoma* SK-MEL-5	2.3	Colon ca. SW480	0.0
Squamous cell	1.9	Colon ca.* (SW480	5.1

carcinoma SCC-4		met) SW620	
Testis Pool	5.1	Colon ca. HT29	8.9
Prostate ca.* (bone met) PC-3	3.6	Colon ca. HCT-116	0.7
Prostate Pool	1.8	Colon ca. CaCo-2	8.1
Placenta	1.4	Colon cancer tissue	8.2
Uterus Pool	2.7	Colon ca. SW1116	0.3
Ovarian ca. OVCAR-3	7.9	Colon ca. Colo-205	1.6
Ovarian ca. SK-OV-3	11.3	Colon ca. SW-48	0.9
Ovarian ca. OVCAR-4	0.8	Colon Pool	10.4
Ovarian ca. OVCAR-5	9.2	Small Intestine Pool	3.6
Ovarian ca. IGROV-1	5.5	Stomach Pool	2.7
Ovarian ca. OVCAR-8	2.0	Bone Marrow Pool	6.3
Ovary	16.7	Fetal Heart	0.9
Breast ca. MCF-7	31.6	Heart Pool	3.8
Breast ca. MDA-MB-231	4.0	Lymph Node Pool	11.9
Breast ca. BT 549	3.7	Fetal Skeletal Muscle	0.4
Breast ca. T47D	20.9	Skeletal Muscle Pool	0.5
Breast ca. MDA-N	0.1	Spleen Pool	10.7
Breast Pool	11.3	Thymus Pool	7.5
Trachea	3.8	CNS cancer (glio/astro) U87-MG	10.2
Lung	9.3	CNS cancer (glio/astro) U-118-MG	1.3
Fetal Lung	3.8	CNS cancer (neuro;met) SK-N-AS	0.1
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF-539	3.0
Lung ca. LX-1	13.8	CNS cancer (astro) SNB-75	10.8
Lung ca. NCI-H146	0.1	CNS cancer (glio) SNB-19	4.9
Lung ca. SHP-77	6.0	CNS cancer (glio) SF-295	21.0
Lung ca. A549	100.0	Brain (Amygdala) Pool	1.1
Lung ca. NCI-H526	0.0	Brain (cerebellum)	2.0
Lung ca. NCI-H23	0.1	Brain (fetal)	1.2

Lung ca. NCI-H460	8.9	Brain (Hippocampus) Pool	1.1
Lung ca. HOP-62	45.4	Cerebral Cortex Pool	1.2
Lung ca. NCI-H522	4.2	Brain (Substantia nigra) Pool	1.3
Liver	0.6	Brain (Thalamus) Pool	1.2
Fetal Liver	1.8	Brain (whole)	1.1
Liver ca. HepG2	1.5	Spinal Cord Pool	1.9
Kidney Pool	8.8	Adrenal Gland	26.8
Fetal Kidney	3.7	Pituitary gland Pool	0.5
Renal ca. 786-0	3.9	Salivary Gland	1.3
Renal ca. A498	10.5	Thyroid (female)	0.7
Renal ca. ACHN	6.2	Pancreatic ca. CAPAN2	20.2
Renal ca. UO-31	6.3	Pancreas Pool	9.6

Table CLD. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag3469, Run 169839390	Tissue Name	Rel. Exp.(%) Ag3469, Run 169839390
Secondary Th1 act	19.2	HUVEC IL-1beta	1.3
Secondary Th2 act	25.2	HUVEC IFN gamma	6.2
Secondary Tr1 act	14.4	HUVEC TNF alpha + IFN gamma	1.3
Secondary Th1 rest	26.1	HUVEC TNF alpha + IL4	1.1
Secondary Th2 rest	46.3	HUVEC IL-11	1.1
Secondary Tr1 rest	36.6	Lung Microvascular EC none	0.7
Primary Th1 act	13.6	Lung Microvascular EC TNFalpha + IL-1beta	0.4
Primary Th2 act	27.7	Microvascular Dermal EC none	0.1
Primary Tr1 act	15.2	Microvascular Dermal EC TNFalpha + IL-1beta	0.0
Primary Th1 rest	46.0	Bronchial epithelium TNFalpha + IL1beta	5.8
Primary Th2 rest	44.4	Small airway epithelium none	2.0
Primary Tr1 rest	45.1	Small airway epithelium TNFalpha + IL-1beta	6.9
CD45RA CD4 lymphocyte act	25.2	Coronary artery SMC rest	3.1
CD45RO CD4 lymphocyte act	67.8	Coronary artery SMC TNFalpha + IL-1beta	3.4

CD8 lymphocyte act	59.5	Astrocytes rest	1.4
Secondary CD8 lymphocyte rest	47.0	Astrocytes TNFalpha + IL-1beta	3.2
Secondary CD8 lymphocyte act	38.4	KU-812 (Basophil) rest	3.0
CD4 lymphocyte none	61.1	KU-812 (Basophil) PMA/ionomycin	6.4
2ry Th1/Th2/Tr1_anti-CD95 CH11	27.2	CCD1106 (Keratinocytes) none	3.8
LAK cells rest	50.7	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	5.2
LAK cells IL-2	36.9	Liver cirrhosis	3.0
LAK cells IL-2+IL-12	49.0	NCI-H292 none	5.0
LAK cells IL-2+IFN gamma	59.5	NCI-H292 IL-4	5.5
LAK cells IL-2+ IL-18	58.2	NCI-H292 IL-9	6.8
LAK cells PMA/ionomycin	65.5	NCI-H292 IL-13	6.7
NK Cells IL-2 rest	47.0	NCI-H292 IFN gamma	8.0
Two Way MLR 3 day	54.0	HPAEC none	2.7
Two Way MLR 5 day	25.2	HPAEC TNF alpha + IL-1 beta	3.3
Two Way MLR 7 day	42.6	Lung fibroblast none	1.5
PBMC rest	23.5	Lung fibroblast TNF alpha + IL-1 beta	1.1
PBMC PWM	37.4	Lung fibroblast IL-4	0.7
PBMC PHA-L	59.5	Lung fibroblast IL-9	3.1
Ramos (B cell) none	1.8	Lung fibroblast IL-13	0.7
Ramos (B cell) ionomycin	2.5	Lung fibroblast IFN gamma	0.3
B lymphocytes PWM	26.8	Dermal fibroblast CCD1070 rest	7.7
B lymphocytes CD40L and IL-4	100.0	Dermal fibroblast CCD1070 TNF alpha	36.9
EOL-1 dbcAMP	2.7	Dermal fibroblast CCD1070 IL-1 beta	5.5
EOL-1 dbcAMP PMA/ionomycin	0.5	Dermal fibroblast IFN gamma	0.7
Dendritic cells none	10.4	Dermal fibroblast IL-4	3.7
Dendritic cells LPS	3.2	Dermal Fibroblasts rest	0.2
Dendritic cells anti-CD40	4.2	Neutrophils TNFa+LPS	0.8
Monocytes rest	1.7	Neutrophils rest	3.2
Monocytes LPS	2.6	Colon	4.4

Macrophages rest	5.6	Lung	5.0
Macrophages LPS	2.6	Thymus	6.9
HUVEC none	0.7	Kidney	2.0
HUVEC starved	1.6		

CNS_neurodegeneration_v1.0 Summary: Ag3469 This panel confirms the expression of the CG59559-01 gene at low levels in the brain in an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. However, as seen in panel 1.4, this gene is expressed at low levels throughout the CNS, including in amygdala, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord. Therefore, this gene may play a role in other central nervous system disorders such as Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

General_screening_panel_v1.4 Summary: Ag3469 Highest expression of the CG59559-01 gene is detected in sample derived from a lung cancer cell line (CT=25.6). Thus, expression of this gene can be used to distinguish this sample from other samples used in this panel. Furthermore, significant expression of this gene is associated with pancreatic cancer, CNS cancer and breast cancer cell lines. Therefore, therapeutic modulation of the activity of this gene or its protein product might be beneficial in the treatment of these cancers.

Among tissues with metabolic function, this gene is expressed in pituitary, adipose, adrenal gland, pancreas, thyroid, and adult and fetal skeletal muscle, heart, and liver. This widespread expression among these tissues suggests that this gene product may play a role in normal neuroendocrine and metabolic and that dysregulated expression of this gene may contribute to neuroendocrine disorders or metabolic diseases, such as obesity and diabetes.

This gene is also expressed at low but significant levels in all regions of the CNS examined. Please see Panel CNS_neurodegeneration_v1.0 for discussion of utility of this gene in the central nervous system.

Panel 4.1D Summary: Ag3469 Highest expression of the CG59559-01 gene is detected in sample derived CD40L and IL-4 treated B lymphocytes (CT=27.2). Furthermore, this gene is expressed at significant levels in a wide range of cell types of significance in the immune response in health and disease. These cells include members of the T-cell, B-cell, endothelial cell, and peripheral blood mononuclear cell family, as well as epithelial and fibroblast cell

types from lung and skin, and normal tissues represented by colon, lung, thymus and kidney. This ubiquitous pattern of expression suggests that this gene product may be involved in homeostatic processes for these and other cell types and tissues. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

CM. CG59669-01: CARBONYL REDUCTASE

Expression of gene CG59669-01 was assessed using the primer-probe set Ag3505, described in Table CMA.

Table CMA. Probe Name Ag3505

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5' - ccgggtcccagaatctagt - 3'	19	4	680
Probe	TET-5' - cctacgccacggttttgaccacg - 3' - TAMRA	23	23	681
Reverse	5' - gacacacggaccacctgat - 3'	19	74	682

CNS_neurodegeneration_v1.0 Summary: Ag3505 Expression of the CG59669-01 gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.4 Summary: Ag3505 Results from one experiment with the CG59669-01 gene are not included. The amp plot indicates that there were experimental difficulties with this run.

Panel 4.1D Summary: Ag3505 Expression of the CG59669-01 gene is low/undetectable (CTs > 35) across all of the samples on this panel due to a probable probe or chemistry failure (data not shown).

Panel 5 Islet Summary: Ag3505 Expression of the CG59669-01 gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

CN. CG59679-01: CARBONYL REDUCTASE

Expression of gene CG59679-01 was assessed using the primer-probe set Ag3507, described in Table CNA.

Table CNA. Probe Name Ag3507

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-gactggagctaataagggcatt-3'	22	130	683
Probe	TET-5'-tcgtgacctgtgtcagcaattctcag-3'- TAMRA	26	166	684
Reverse	5'-gtgcagtgagcaccacatc-3'	19	194	685

CNS_neurodegeneration_v1.0 Summary: Ag3507 Expression of the CG59679-01 gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.4 Summary: Ag3507 Expression of the CG59679-01 gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Panel 4.1D Summary: Ag3507 Expression of the CG59679-01 gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown). The data suggest that there may have been experimental difficulties with this run.

Panel 5 Islet Summary: Ag3507 Expression of CG59679-01 gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

CO. CG59644-01: Putative protein phosphatase

Expression of gene CG59644-01 was assessed using the primer-probe set Ag3503, described in Table COA. Results of the RTQ-PCR runs are shown in Tables COB, COC and COD.

Table COA. Probe Name Ag3503

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-tcgtacctagtaatccgattgg-3'	22	410	763
Probe	TET-5'-ccacaagctactgtgagttgctgcaa-3'- TAMRA	26	440	764
Reverse	5'-ctaccgagcaaagggactttat-3'	22	467	765

Table COB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3503, Run 210938272	Tissue Name	Rel. Exp.(%) Ag3503, Run 210938272
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AD 1 Hippo	22.1	Control (Path) 3 Temporal Ctx	5.7
AD 2 Hippo	29.1	Control (Path) 4 Temporal Ctx	25.3
AD 3 Hippo	10.8	AD 1 Occipital Ctx	21.8
AD 4 Hippo	9.4	AD 2 Occipital Ctx (Missing)	0.0
AD 5 hippo	100.0	AD 3 Occipital Ctx	8.9
AD 6 Hippo	80.7	AD 4 Occipital Ctx	22.8
Control 2 Hippo	27.0	AD 5 Occipital Ctx	26.8
Control 4 Hippo	11.4	AD 6 Occipital Ctx	56.6
Control (Path) 3 Hippo	11.3	Control 1 Occipital Ctx	5.6
AD 1 Temporal Ctx	18.9	Control 2 Occipital Ctx	93.3
AD 2 Temporal Ctx	29.5	Control 3 Occipital Ctx	15.8
AD 3 Temporal Ctx	7.2	Control 4 Occipital Ctx	6.1
AD 4 Temporal Ctx	19.3	Control (Path) 1 Occipital Ctx	80.1
AD 5 Inf Temporal Ctx	73.2	Control (Path) 2 Occipital Ctx	7.5
AD 5 Sup Temporal Ctx	49.0	Control (Path) 3 Occipital Ctx	5.9
AD 6 Inf Temporal Ctx	68.8	Control (Path) 4 Occipital Ctx	14.5
AD 6 Sup Temporal Ctx	66.0	Control 1 Parietal Ctx	7.6
Control 1 Temporal Ctx	4.4	Control 2 Parietal Ctx	29.1
Control 2 Temporal Ctx	53.2	Control 3 Parietal Ctx	26.6
Control 3 Temporal Ctx	9.7	Control (Path) 1 Parietal Ctx	95.9
Control 4 Temporal Ctx	11.3	Control (Path) 2 Parietal Ctx	22.5
Control (Path) 1 Temporal Ctx	48.0	Control (Path) 3 Parietal Ctx	6.8
Control (Path) 2 Temporal Ctx	22.2	Control (Path) 4 Parietal Ctx	49.7

Table COC. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3503,	Tissue Name	Rel. Exp.(%) Ag3503,
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	Run 217131685		Run 217131685
Adipose	12.9	Renal ca. TK-10	26.8
Melanoma* Hs688(A).T	7.7	Bladder	22.1
Melanoma* Hs688(B).T	11.0	Gastric ca. (liver met.) NCI-N87	63.7
Melanoma* M14	25.0	Gastric ca. KATO III	66.0
Melanoma* LOXIMVI	25.9	Colon ca. SW-948	16.4
Melanoma* SK- MEL-5	69.3	Colon ca. SW480	37.4
Squamous cell carcinoma SCC-4	18.9	Colon ca.* (SW480 met) SW620	24.8
Testis Pool	13.0	Colon ca. HT29	13.7
Prostate ca.* (bone met) PC-3	51.8	Colon ca. HCT-116	60.3
Prostate Pool	6.9	Colon ca. CaCo-2	25.7
Placenta	7.1	Colon cancer tissue	34.9
Uterus Pool	5.9	Colon ca. SW1116	8.2
Ovarian ca. OVCAR-3	14.0	Colon ca. Colo-205	9.2
Ovarian ca. SK-OV- 3	90.8	Colon ca. SW-48	5.8
Ovarian ca. OVCAR-4	12.5	Colon Pool	17.4
Ovarian ca. OVCAR-5	34.2	Small Intestine Pool	15.7
Ovarian ca. IGROV- 1	33.0	Stomach Pool	6.6
Ovarian ca. OVCAR-8	17.6	Bone Marrow Pool	6.4
Ovary	7.8	Fetal Heart	12.1
Breast ca. MCF-7	15.9	Heart Pool	17.7
Breast ca. MDA- MB-231	55.1	Lymph Node Pool	17.6
Breast ca. BT 549	19.8	Fetal Skeletal Muscle	4.8
Breast ca. T47D	66.9	Skeletal Muscle Pool	100.0
Breast ca. MDA-N	12.2	Spleen Pool	12.5
Breast Pool	17.6	Thymus Pool	14.2
Trachea	28.7	CNS cancer (glio/astro) U87-MG	42.9
Lung	3.0	CNS cancer (glio/astro) U-118-MG	55.1
Fetal Lung	18.8	CNS cancer	30.6

		(neuro;met) SK-N-AS	
Lung ca. NCI-N417	9.1	CNS cancer (astro) SF-539	12.2
Lung ca. LX-1	41.2	CNS cancer (astro) SNB-75	22.4
Lung ca. NCI-H146	7.0	CNS cancer (glio) SNB-19	36.3
Lung ca. SHP-77	26.8	CNS cancer (glio) SF-295	50.7
Lung ca. A549	24.8	Brain (Amygdala) Pool	12.4
Lung ca. NCI-H526	8.0	Brain (cerebellum)	14.6
Lung ca. NCI-H23	26.6	Brain (fetal)	10.2
Lung ca. NCI-H460	29.7	Brain (Hippocampus) Pool	13.8
Lung ca. HOP-62	8.0	Cerebral Cortex Pool	17.2
Lung ca. NCI-H522	19.9	Brain (Substantia nigra) Pool	19.1
Liver	2.9	Brain (Thalamus) Pool	18.4
Fetal Liver	10.4	Brain (whole)	15.7
Liver ca. HepG2	14.2	Spinal Cord Pool	10.9
Kidney Pool	23.8	Adrenal Gland	25.7
Fetal Kidney	10.4	Pituitary gland Pool	3.9
Renal ca. 786-0	12.3	Salivary Gland	11.1
Renal ca. A498	3.7	Thyroid (female)	4.4
Renal ca. ACHN	27.9	Pancreatic ca. CAPAN2	15.0
Renal ca. UO-31	12.0	Pancreas Pool	17.1

Table COD. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3503, Run 166441943	Tissue Name	Rel. Exp.(%) Ag3503, Run 166441943
Secondary Th1 act	54.3	HUVEC IL-1beta	20.4
Secondary Th2 act	52.5	HUVEC IFN gamma	14.6
Secondary Tr1 act	61.1	HUVEC TNF alpha + IFN gamma	16.0
Secondary Th1 rest	34.6	HUVEC TNF alpha + IL4	24.8
Secondary Th2 rest	20.0	HUVEC IL-11	6.6
Secondary Tr1 rest	23.0	Lung Microvascular EC none	12.9
Primary Th1 act	39.5	Lung Microvascular EC TNFalpha + IL-1beta	17.4
Primary Th2 act	59.9	Microvascular Dermal EC none	21.6

Primary Tr1 act	92.7	Microsvascular Dermal EC TNFalpha + IL-1beta	20.2
Primary Th1 rest	94.6	Bronchial epithelium TNFalpha + IL1beta	17.7
Primary Th2 rest	31.4	Small airway epithelium none	7.9
Primary Tr1 rest	32.8	Small airway epithelium TNFalpha + IL-1beta	53.6
CD45RA CD4 lymphocyte act	44.1	Coronary artery SMC rest	7.7
CD45RO CD4 lymphocyte act	65.5	Coronary artery SMC TNFalpha + IL-1beta	8.3
CD8 lymphocyte act	68.3	Astrocytes rest	11.7
Secondary CD8 lymphocyte rest	68.8	Astrocytes TNFalpha + IL-1beta	21.9
Secondary CD8 lymphocyte act	40.1	KU-812 (Basophil) rest	12.1
CD4 lymphocyte none	20.9	KU-812 (Basophil) PMA/ionomycin	42.6
2ry Th1/Th2/Tr1_anti- CD95 CH11	40.9	CCD1106 (Keratinocytes) none	21.0
LAK cells rest	22.7	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	72.2
LAK cells IL-2	46.7	Liver cirrhosis	12.8
LAK cells IL-2+IL-12	38.2	Lupus kidney	16.7
LAK cells IL-2+IFN gamma	68.8	NCI-H292 none	33.0
LAK cells IL-2+ IL-18	57.8	NCI-H292 IL-4	35.1
LAK cells PMA/ionomycin	100.0	NCI-H292 IL-9	35.4
NK Cells IL-2 rest	32.8	NCI-H292 IL-13	24.8
Two Way MLR 3 day	42.9	NCI-H292 IFN gamma	22.5
Two Way MLR 5 day	39.8	HPAEC none	11.2
Two Way MLR 7 day	33.7	HPAEC TNF alpha + IL-1 beta	27.9
PBMC rest	22.5	Lung fibroblast none	10.6
PBMC PWM	54.0	Lung fibroblast TNF alpha + IL-1 beta	25.5
PBMC PHA-L	20.6	Lung fibroblast IL-4	11.6
Ramos (B cell) none	56.3	Lung fibroblast IL-9	5.4
Ramos (B cell) ionomycin	38.4	Lung fibroblast IL-13	8.5
B lymphocytes PWM	44.8	Lung fibroblast IFN gamma	11.7
B lymphocytes CD40L	42.9	Dermal fibroblast	16.4

and IL-4		CCD1070 rest	
EOL-1 dbcAMP	18.2	Dermal fibroblast CCD1070 TNF alpha	56.3
EOL-1 dbcAMP PMA/ionomycin	30.4	Dermal fibroblast CCD1070 IL-1 beta	14.4
Dendritic cells none	31.2	Dermal fibroblast IFN gamma	14.5
Dendritic cells LPS	40.9	Dermal fibroblast IL-4	29.1
Dendritic cells anti- CD40	31.2	IBD Colitis 2	13.7
Monocytes rest	50.0	IBD Crohn's	11.6
Monocytes LPS	31.0	Colon	70.7
Macrophages rest	26.4	Lung	17.1
Macrophages LPS	28.9	Thymus	29.3
HUVEC none	22.2	Kidney	40.1
HUVEC starved	25.3		

CNS_neurodegeneration_v1.0 Summary: Ag3503 This panel confirms the expression of this gene at low levels in the brains of an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. Please see Panel 1.4 for a discussion of the potential utility of this gene in treatment of central nervous system disorders.

General_screening_panel_v1.4 Summary: Ag3503 Expression of the CG59644-01 gene is highest in adult skeletal muscle (CT = 25.5). Interestingly, expression of this gene is much lower in fetal skeletal muscle (CT = 29.9), suggesting that expression of this gene may be used to distinguish adult and fetal skeletal muscle.

The CG59644-01 gene encodes a protein with homology to protein phosphatases. This gene is expressed at high to moderate levels in the majority of samples on this panel. However, expression of this gene appears to be higher in cancer cell lines when compared to normal adult tissues. This observation is consistent with the potential role for this gene product in cell survival and proliferation.

In addition, this gene is expressed at high levels in all regions of the central nervous system examined, including amygdala, hippocampus, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord. Therefore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

Among tissues with metabolic or endocrine function, this gene is expressed at high to moderate levels in pancreas, adipose, adrenal gland, thyroid, pituitary gland, skeletal muscle, heart, liver and the gastrointestinal tract. Therefore, therapeutic modulation of the activity of this gene may prove useful in the treatment of endocrine/metabolically related diseases, such as obesity and diabetes.

Panel 4D Summary: Ag3503 This gene is expressed at high to moderate levels in a wide range of cell types of significance in the immune response in health and disease. These cells include T cells, B cells, endothelial cells, macrophages, monocytes, dendritic cells, basophils, eosinophils and peripheral blood mononuclear cells, as well as epithelial and fibroblast cell types from lung and skin, and normal tissues represented by colon, lung, thymus and kidney. This ubiquitous pattern of expression suggests that this gene product may be involved in homeostatic processes for these and other cell types and tissues. This pattern is in agreement with the expression profile in General_screening_panel_v1.5 and also suggests a role for the gene product in cell survival and proliferation. Therefore, therapeutic modulation of the activity of this gene or its protein product may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

CP. CG59662-01: Cyclophilin

Expression of gene CG59662-01 was assessed using the primer-probe set Ag3504, described in Table CPA. Results of the RTQ-PCR runs are shown in Tables CPB and CPC.

Table CPA. Probe Name Ag3504

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-ggcacaaccacaccatgttctt-3'	21	22	686
Probe	TET-5'-cttggaaccacgtctcctttgagctg-3'-TAMRA	25	67	687
Reverse	5'-tctttggaaacttttctgcaaa-3'	22	92	688

Table CPB. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3504, Run 217236170	Tissue Name	Rel. Exp.(%) Ag3504, Run 217236170
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Adipose	0.5	Renal ca. TK-10	0.4
Melanoma* Hs688(A).T	1.0	Bladder	0.6
Melanoma* Hs688(B).T	0.4	Gastric ca. (liver met.) NCI-N87	4.8
Melanoma* M14	100.0	Gastric ca. KATO III	14.2
Melanoma* LOXIMVI	3.9	Colon ca. SW-948	2.3
Melanoma* SK- MEL-5	4.9	Colon ca. SW480	12.9
Squamous cell carcinoma SCC-4	47.6	Colon ca.* (SW480 met) SW620	0.3
Testis Pool	2.7	Colon ca. HT29	3.5
Prostate ca.* (bone met) PC-3	3.1	Colon ca. HCT-116	1.1
Prostate Pool	5.7	Colon ca. CaCo-2	11.6
Placenta	5.0	Colon cancer tissue	7.6
Uterus Pool	2.2	Colon ca. SW1116	1.5
Ovarian ca. OVCAR-3	20.6	Colon ca. Colo-205	11.7
Ovarian ca. SK-OV- 3	6.3	Colon ca. SW-48	6.2
Ovarian ca. OVCAR-4	1.5	Colon Pool	4.7
Ovarian ca. OVCAR-5	10.2	Small Intestine Pool	2.5
Ovarian ca. IGROV- 1	0.6	Stomach Pool	5.8
Ovarian ca. OVCAR-8	0.7	Bone Marrow Pool	1.2
Ovary	2.2	Fetal Heart	3.3
Breast ca. MCF-7	2.9	Heart Pool	2.2
Breast ca. MDA- MB-231	4.0	Lymph Node Pool	11.8
Breast ca. BT 549	5.6	Fetal Skeletal Muscle	0.9
Breast ca. T47D	15.0	Skeletal Muscle Pool	32.3
Breast ca. MDA-N	17.7	Spleen Pool	2.0
Breast Pool	0.9	Thymus Pool	9.3
Trachea	2.0	CNS cancer (glio/astro) U87-MG	1.0
Lung	16.3	CNS cancer (glio/astro) U-118-MG	3.3
Fetal Lung	42.0	CNS cancer (neuro;met) SK-N-AS	6.2

Lung ca. NCI-N417	3.6	CNS cancer (astro) SF-539	2.3
Lung ca. LX-1	0.7	CNS cancer (astro) SNB-75	12.7
Lung ca. NCI-H146	5.1	CNS cancer (glio) SNB-19	4.1
Lung ca. SHP-77	17.6	CNS cancer (glio) SF-295	0.7
Lung ca. A549	19.9	Brain (Amygdala) Pool	3.3
Lung ca. NCI-H526	4.3	Brain (cerebellum)	2.3
Lung ca. NCI-H23	3.3	Brain (fetal)	0.9
Lung ca. NCI-H460	3.8	Brain (Hippocampus) Pool	16.3
Lung ca. HOP-62	0.7	Cerebral Cortex Pool	0.5
Lung ca. NCI-H522	1.5	Brain (Substantia nigra) Pool	4.6
Liver	1.2	Brain (Thalamus) Pool	9.0
Fetal Liver	17.2	Brain (whole)	1.4
Liver ca. HepG2	1.2	Spinal Cord Pool	11.6
Kidney Pool	5.1	Adrenal Gland	0.3
Fetal Kidney	7.1	Pituitary gland Pool	3.9
Renal ca. 786-0	1.2	Salivary Gland	1.2
Renal ca. A498	2.4	Thyroid (female)	5.5
Renal ca. ACHN	1.2	Pancreatic ca. CAPAN2	0.6
Renal ca. UO-31	2.5	Pancreas Pool	8.8

Table CPC. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3504, Run 166407168	Tissue Name	Rel. Exp.(%) Ag3504, Run 166407168
Secondary Th1 act	0.0	HUVEC IL-1beta	0.0
Secondary Th2 act	0.0	HUVEC IFN gamma	0.0
Secondary Tr1 act	0.0	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	0.0	HUVEC IL-11	0.0
Secondary Tr1 rest	0.0	Lung Microvascular EC none	0.0
Primary Th1 act	0.0	Lung Microvascular EC TNFalpha + IL-1beta	0.0
Primary Th2 act	0.0	Microvascular Dermal EC none	0.0
Primary Tr1 act	0.0	Microvascular Dermal EC	0.0

		TNFAIpha + IL-1beta	
Primary Th1 rest	0.0	Bronchial epithelium TNFAIpha + IL1beta	0.0
Primary Th2 rest	0.0	Small airway epithelium none	0.0
Primary Tr1 rest	0.0	Small airway epithelium TNFAIpha + IL-1beta	0.0
CD45RA CD4 lymphocyte act	0.0	Coronary artery SMC rest	0.0
CD45RO CD4 lymphocyte act	0.0	Coronary artery SMC TNFAIpha + IL-1beta	0.0
CD8 lymphocyte act	0.0	Astrocytes rest	0.0
Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFAIpha + IL-1beta	0.0
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	0.0
2ry Th1/Th2/Tr1_anti- CD95 CH11	0.0	CCD1106 (Keratinocytes) none	0.0
LAK cells rest	0.0	CCD1106 (Keratinocytes) TNFAIpha + IL-1beta	0.0
LAK cells IL-2	0.0	Liver cirrhosis	100.0
LAK cells IL-2+IL-12	0.0	Lupus kidney	0.0
LAK cells IL-2+IFN gamma	0.0	NCI-H292 none	0.0
LAK cells IL-2+ IL-18	0.0	NCI-H292 IL-4	0.0
LAK cells PMA/ionomycin	0.0	NCI-H292 IL-9	0.0
NK Cells IL-2 rest	0.0	NCI-H292 IL-13	0.0
Two Way MLR 3 day	0.0	NCI-H292 IFN gamma	0.0
Two Way MLR 5 day	0.0	HPAEC none	0.0
Two Way MLR 7 day	0.0	HPAEC TNF alpha + IL-1 beta	0.0
PBMC rest	0.0	Lung fibroblast none	0.0
PBMC PWM	0.0	Lung fibroblast TNF alpha + IL-1 beta	0.0
PBMC PHA-L	0.0	Lung fibroblast IL-4	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-9	0.0
Ramos (B cell) ionomycin	0.0	Lung fibroblast IL-13	0.0
B lymphocytes PWM	0.0	Lung fibroblast IFN gamma	3.5
B lymphocytes CD40L and IL-4	0.0	Dermal fibroblast CCD1070 rest	0.0

EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 TNF alpha	0.0
EOL-1 dbcAMP PMA/ionomycin	0.0	Dermal fibroblast CCD1070 IL-1 beta	0.0
Dendritic cells none	0.0	Dermal fibroblast IFN gamma	2.7
Dendritic cells LPS	0.0	Dermal fibroblast IL-4	0.0
Dendritic cells anti- CD40	0.0	IBD Colitis 2	3.6
Monocytes rest	0.0	IBD Crohn's	0.0
Monocytes LPS	0.0	Colon	17.0
Macrophages rest	0.0	Lung	2.2
Macrophages LPS	0.0	Thymus	9.0
HUVEC none	0.0	Kidney	0.0
HUVEC starved	0.0		

CNS_neurodegeneration_v1.0 Summary: Ag3504 Expression of the CG59662-01 gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.4 Summary: Ag3504 The CG59662-01 gene is expressed at low levels in the majority of samples on this panel, with highest expression in a melanoma cell line (CT = 30). The CG59662-01 gene encodes a protein with homology to cyclophilin, a specific high-affinity binding protein for the immunosuppressant agent cyclosporin A.

Among tissues with metabolic or endocrine function, this gene is expressed at low levels in pancreas, thyroid, pituitary gland, skeletal muscle, heart, liver and the gastrointestinal tract. Therefore, therapeutic modulation of the activity of this gene may prove useful in the treatment of endocrine/metabolically related diseases, such as obesity and diabetes. Interestingly, this gene is expressed at higher levels in fetal liver (CT = 32.5) than in adult liver (CT = 36.4), suggesting that expression of this gene can be used to distinguish fetal and adult liver.

In addition, this gene is expressed at low levels in some regions of the central nervous system, including amygdala, hippocampus, substantia nigra, thalamus, and spinal cord. Therefore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

Panel 4D Summary: Ag3504 Significant expression of this gene is detected in a liver cirrhosis sample (CT = 34.4). Furthermore, expression of this gene is not detected at

significant levels in normal adult liver in Panel 1.4, suggesting that its expression is unique to liver cirrhosis. This gene encodes a putative cyclophilin; therefore, small molecule therapeutics could reduce or inhibit fibrosis that occurs in liver cirrhosis. In addition, expression of this putative cyclophilin could also be used for the diagnosis of liver cirrhosis.

CQ. CG59773-01: splice variant of myomegalin

Expression of gene CG59773-01 was assessed using the primer-probe set Ag3580, described in Table CQA. Results of the RTQ-PCR runs are shown in Tables CQB, CQC and CQD.

Table CQA. Probe Name Ag3580

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-tggagttagttccggtttcc-3'	20	1647	689
Probe	TET-5'-tgaaacccctttacaagacacctgtg-3'-TAMRA	26	1679	690
Reverse	5'-ctgaaagctccaagggataact-3'	22	1705	691

Table CQB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3580, Run 210643837	Rel. Exp.(%) Ag3580, Run 224078543	Tissue Name	Rel. Exp.(%) Ag3580, Run 210643837	Rel. Exp.(%) Ag3580, Run 224078543
AD 1 Hippo	28.9	31.0	Control (Path) 3 Temporal Ctx	5.9	4.8
AD 2 Hippo	20.9	19.9	Control (Path) 4 Temporal Ctx	19.9	19.2
AD 3 Hippo	10.7	9.7	AD 1 Occipital Ctx	26.1	20.3
AD 4 Hippo	5.4	4.4	AD 2 Occipital Ctx (Missing)	0.0	0.0
AD 5 Hippo	100.0	100.0	AD 3 Occipital Ctx	9.9	8.8
AD 6 Hippo	78.5	62.4	AD 4	13.5	13.2

			Occipital Ctx		
Control 2 Hippo	15.3	14.6	AD 5 Occipital Ctx	19.6	16.6
Control 4 Hippo	13.5	12.1	AD 6 Occipital Ctx	18.4	17.9
Control (Path) 3 Hippo	7.6	7.5	Control 1 Occipital Ctx	2.3	2.1
AD 1 Temporal Ctx	38.2	29.7	Control 2 Occipital Ctx	31.2	29.3
AD 2 Temporal Ctx	24.8	20.7	Control 3 Occipital Ctx	10.5	9.5
AD 3 Temporal Ctx	13.2	9.1	Control 4 Occipital Ctx	7.7	7.2
AD 4 Temporal Ctx	16.5	17.6	Control (Path) 1 Occipital Ctx	47.6	48.3
AD 5 Inf Temporal Ctx	89.5	81.2	Control (Path) 2 Occipital Ctx	8.0	7.2
AD 5 Sup Temporal Ctx	66.0	63.7	Control (Path) 3 Occipital Ctx	2.9	2.3
AD 6 Inf Temporal Ctx	47.3	45.1	Control (Path) 4 Occipital Ctx	9.9	9.1
AD 6 Sup Temporal Ctx	41.8	38.4	Control 1 Parietal Ctx	5.4	5.1
Control 1 Temporal Ctx	4.6	4.5	Control 2 Parietal Ctx	67.8	59.0
Control 2 Temporal Ctx	17.6	14.5	Control 3 Parietal Ctx	9.8	8.4
Control 3 Temporal	9.0	8.5	Control (Path) 1	40.6	35.8

Ctx			Parietal Ctx		
Control 3 Temporal Ctx	6.0	5.9	Control (Path) 2 Parietal Ctx	15.2	14.1
Control (Path) 1 Temporal Ctx	29.1	27.4	Control (Path) 3 Parietal Ctx	4.9	3.2
Control (Path) 2 Temporal Ctx	22.1	20.6	Control (Path) 4 Parietal Ctx	24.1	23.8

Table CQC. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3580, Run 217423587	Tissue Name	Rel. Exp.(%) Ag3580, Run 217423587
Adipose	20.7	Renal ca. TK-10	20.7
Melanoma* Hs688(A).T	76.8	Bladder	15.7
Melanoma* Hs688(B).T	38.7	Gastric ca. (liver met.) NCI-N87	50.0
Melanoma* M14	7.6	Gastric ca. KATO III	13.1
Melanoma* LOXIMVI	81.2	Colon ca. SW-948	5.8
Melanoma* SK- MEL-5	14.9	Colon ca. SW480	12.9
Squamous cell carcinoma SCC-4	10.2	Colon ca.* (SW480 met) SW620	2.6
Testis Pool	4.5	Colon ca. HT29	4.5
Prostate ca.* (bone met) PC-3	29.1	Colon ca. HCT-116	15.0
Prostate Pool	6.1	Colon ca. CaCo-2	29.7
Placenta	8.2	Colon cancer tissue	8.4
Uterus Pool	7.7	Colon ca. SW1116	2.5
Ovarian ca. OVCAR-3	24.0	Colon ca. Colo-205	2.9
Ovarian ca. SK-OV- 3	15.4	Colon ca. SW-48	7.1
Ovarian ca. OVCAR-4	17.0	Colon Pool	18.8
Ovarian ca. OVCAR-5	19.8	Small Intestine Pool	18.0
Ovarian ca. IGROV- 1	15.1	Stomach Pool	7.4

Ovarian ca. OVCAR-8	6.7	Bone Marrow Pool	9.9
Ovary	4.4	Fetal Heart	9.0
Breast ca. MCF-7	28.9	Heart Pool	8.2
Breast ca. MDA-MB-231	39.8	Lymph Node Pool	22.8
Breast ca. BT 549	13.9	Fetal Skeletal Muscle	6.8
Breast ca. T47D	49.0	Skeletal Muscle Pool	22.7
Breast ca. MDA-N	7.6	Spleen Pool	12.1
Breast Pool	9.5	Thymus Pool	19.9
Trachea	15.0	CNS cancer (glio/astro) U87-MG	35.1
Lung	4.0	CNS cancer (glio/astro) U-118-MG	28.9
Fetal Lung	30.6	CNS cancer (neuro;met) SK-N-AS	3.4
Lung ca. NCI-N417	5.4	CNS cancer (astro) SF-539	13.4
Lung ca. LX-1	6.6	CNS cancer (astro) SNB-75	57.4
Lung ca. NCI-H146	15.8	CNS cancer (glio) SNB-19	9.0
Lung ca. SHP-77	25.9	CNS cancer (glio) SF-295	49.7
Lung ca. A549	4.2	Brain (Amygdala) Pool	15.9
Lung ca. NCI-H526	7.6	Brain (cerebellum)	100.0
Lung ca. NCI-H23	50.0	Brain (fetal)	69.3
Lung ca. NCI-H460	4.8	Brain (Hippocampus) Pool	16.0
Lung ca. HOP-62	24.3	Cerebral Cortex Pool	26.1
Lung ca. NCI-H522	4.5	Brain (Substantia nigra) Pool	22.7
Liver	4.9	Brain (Thalamus) Pool	37.4
Fetal Liver	12.0	Brain (whole)	33.4
Liver ca. HepG2	11.1	Spinal Cord Pool	34.4
Kidney Pool	54.0	Adrenal Gland	5.2
Fetal Kidney	40.3	Pituitary gland Pool	9.7
Renal ca. 786-0	13.9	Salivary Gland	3.4
Renal ca. A498	15.0	Thyroid (female)	5.3
Renal ca. ACHN	1.6	Pancreatic ca. CAPAN2	16.4
Renal ca. UO-31	10.2	Pancreas Pool	17.2

Table CQD. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag3580, Run 169910382	Tissue Name	Rel. Exp.(%) Ag3580, Run 169910382
Secondary Th1 act	28.3	HUVEC IL-1beta	28.5
Secondary Th2 act	32.8	HUVEC IFN gamma	8.0
Secondary Tr1 act	34.2	HUVEC TNF alpha + IFN gamma	30.1
Secondary Th1 rest	23.7	HUVEC TNF alpha + IL4	27.2
Secondary Th2 rest	26.4	HUVEC IL-11	8.8
Secondary Tr1 rest	34.2	Lung Microvascular EC none	42.9
Primary Th1 act	11.2	Lung Microvascular EC TNFalpha + IL-1beta	33.2
Primary Th2 act	10.8	Microvascular Dermal EC none	24.8
Primary Tr1 act	11.0	Microvascular Dermal EC TNFalpha + IL-1beta	20.7
Primary Th1 rest	32.3	Bronchial epithelium TNFalpha + IL1beta	18.6
Primary Th2 rest	31.2	Small airway epithelium none	8.2
Primary Tr1 rest	24.1	Small airway epithelium TNFalpha + IL-1beta	10.7
CD45RA CD4 lymphocyte act	50.0	Coronary artery SMC rest	10.7
CD45RO CD4 lymphocyte act	25.5	Coronary artery SMC TNFalpha + IL-1beta	15.6
CD8 lymphocyte act	18.8	Astrocytes rest	14.1
Secondary CD8 lymphocyte rest	16.3	Astrocytes TNFalpha + IL-1beta	13.0
Secondary CD8 lymphocyte act	16.3	KU-812 (Basophil) rest	4.0
CD4 lymphocyte none	22.4	KU-812 (Basophil) PMA/ionomycin	7.8
2ry Th1/Th2/Tr1 _anti- CD95 CH11	47.6	CCD1106 (Keratinocytes) none	24.3
LAK cells rest	24.1	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	26.4
LAK cells IL-2	21.8	Liver cirrhosis	12.0
LAK cells IL-2+IL-12	23.2	NCI-H292 none	9.6
LAK cells IL-2+IFN gamma	29.1	NCI-H292 IL-4	15.5
LAK cells IL-2+ IL-18	32.5	NCI-H292 IL-9	26.2
LAK cells PMA/ionomycin	35.8	NCI-H292 IL-13	15.3

NK Cells IL-2 rest	26.1	NCI-H292 IFN gamma	14.0
Two Way MLR 3 day	35.8	HPAEC none	8.2
Two Way MLR 5 day	19.5	HPAEC TNF alpha + IL-1 beta	31.9
Two Way MLR 7 day	46.0	Lung fibroblast none	51.8
PBMC rest	15.8	Lung fibroblast TNF alpha + IL-1 beta	44.8
PBMC PWM	16.0	Lung fibroblast IL-4	32.8
PBMC PHA-L	13.3	Lung fibroblast IL-9	51.4
Ramos (B cell) none	16.8	Lung fibroblast IL-13	29.9
Ramos (B cell) ionomycin	15.9	Lung fibroblast IFN gamma	27.7
B lymphocytes PWM	14.4	Dermal fibroblast CCD1070 rest	38.4
B lymphocytes CD40L and IL-4	16.3	Dermal fibroblast CCD1070 TNF alpha	100.0
EOL-1 dbcAMP	5.6	Dermal fibroblast CCD1070 IL-1 beta	48.3
EOL-1 dbcAMP PMA/ionomycin	29.3	Dermal fibroblast IFN gamma	11.0
Dendritic cells none	13.6	Dermal fibroblast IL-4	22.7
Dendritic cells LPS	14.4	Dermal Fibroblasts rest	18.8
Dendritic cells anti-CD40	13.5	Neutrophils TNFa+LPS	1.7
Monocytes rest	12.3	Neutrophils rest	2.6
Monocytes LPS	62.9	Colon	15.8
Macrophages rest	18.4	Lung	15.6
Macrophages LPS	15.3	Thymus	21.8
HUVEC none	12.6	Kidney	46.3
HUVEC starved	17.0		

CNS_neurodegeneration_v1.0 Summary: Ag3580 Results from two experiments using the same probe/primer set are in excellent agreement. This panel confirms the expression of this gene at high to moderate levels in the brains of an independent group of individuals. This gene is found to be upregulated in the temporal cortex of Alzheimer's disease patients. Therefore, therapeutic modulation of this gene or its protein product may be used to decrease neuronal death and treat Alzheimer's disease.

General_screening_panel_v1.4 Summary: Ag3580 The CG59773-01 gene encodes a splice variant of the myomegalin protein, which is a component of the golgi/centrosome and interacts with a cyclic nucleotide phosphodiesterase (ref. 1). Expression of the CG59773-01 gene is

highest in the cerebellum (CT = 23.8). In addition, this gene is expressed at high levels in all other regions of the central nervous system examined, including amygdala, hippocampus, substantia nigra, thalamus, cerebral cortex, and spinal cord. Therefore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

Among tissues with metabolic or endocrine function, this gene is expressed at high to moderate levels in pancreas, adipose, adrenal gland, thyroid, pituitary gland, skeletal muscle, heart, liver and the gastrointestinal tract. Therefore, therapeutic modulation of the activity of this gene may prove useful in the treatment of endocrine/metabolically related diseases, such as obesity and diabetes.

This gene is also expressed at very high levels in a number of melanoma cell lines. Therefore, therapeutic modulation of the activity of this gene or its protein product may be of benefit in the treatment of melanoma.

References:

1. Verde I, Pahlke G, Salanova M, Zhang G, Wang S, Coletti D, Onuffer J, Jin SL, Conti M. Myomegalin is a novel protein of the golgi/centrosome that interacts with a cyclic nucleotide phosphodiesterase. J Biol Chem 2001 Apr 6;276(14):11189-98

Panel 4.1D Summary: Ag3580 This gene is expressed at high to moderate levels in a wide range of cell types of significance in the immune response in health and disease. These cells include T cells, B cells, endothelial cells, macrophages, monocytes, dendritic cells, basophils, eosinophils and peripheral blood mononuclear cells, as well as epithelial and fibroblast cell types from lung and skin, and normal tissues represented by colon, lung, thymus and kidney. This ubiquitous pattern of expression suggests that this gene product may be involved in homeostatic processes for these and other cell types and tissues. This pattern is in agreement with the expression profile in General_screening_panel_v1.5 and also suggests a role for the gene product in cell survival and proliferation. Therefore, therapeutic modulation of the activity of this gene or its protein product may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

CR. CG57460-01: N-ACETYLTRANSFERASE CAMELLO 2

Expression of gene CG57460-01 was assessed using the primer-probe set Ag3273, described in Table CRA. Results of the RTQ-PCR runs are shown in Tables CRB, CRC and CRD.

Table CRA. Probe Name Ag3273

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5' - cgctactactacagccgcaa - 3'	20	205	692
Probe	TET-5' - gtgatccgcgcctacctggagtg - 3' - TAMRA	23	226	693
Reverse	5' - gggcggccttcattgtagtact - 3'	20	281	694

Table CRB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3273, Run 210038591	Rel. Exp.(%) Ag3273, Run 230512515	Tissue Name	Rel. Exp.(%) Ag3273, Run 210038591	Rel. Exp.(%) Ag3273, Run 230512515
AD 1 Hippo	15.7	18.6	Control (Path) 3 Temporal Ctx	12.2	12.7
AD 2 Hippo	28.9	23.2	Control (Path) 4 Temporal Ctx	40.3	35.4
AD 3 Hippo	11.0	11.0	AD 1 Occipital Ctx	20.9	18.8
AD 4 Hippo	10.2	13.8	AD 2 Occipital Ctx (Missing)	0.0	0.0
AD 5 hippo	100.0	100.0	AD 3 Occipital Ctx	15.2	13.1
AD 6 Hippo	21.8	22.4	AD 4 Occipital Ctx	22.1	23.2
Control 2 Hippo	27.0	27.9	AD 5 Occipital Ctx	18.4	18.4
Control 4	22.5	21.8	AD 6	46.3	48.3

Hippo			Occipital Ctx		
Control (Path) 3 Hippo	8.4	9.0	Control 1 Occipital Ctx	8.0	11.2
AD 1 Temporal Ctx	16.5	15.1	Control 2 Occipital Ctx	80.1	82.4
AD 2 Temporal Ctx	29.3	26.2	Control 3 Occipital Ctx	26.2	27.2
AD 3 Temporal Ctx	10.9	12.9	Control 4 Occipital Ctx	14.8	14.1
AD 4 Temporal Ctx	22.5	20.3	Control (Path) 1 Occipital Ctx	70.2	68.8
AD 5 Inf Temporal Ctx	57.0	59.5	Control (Path) 2 Occipital Ctx	21.6	20.6
AD 5 Sup Temporal Ctx	30.6	26.8	Control (Path) 3 Occipital Ctx	8.8	7.4
AD 6 Inf Temporal Ctx	27.2	30.1	Control (Path) 4 Occipital Ctx	36.1	34.2
AD 6 Sup Temporal Ctx	34.2	37.4	Control 1 Parietal Ctx	14.1	13.7
Control 1 Temporal Ctx	12.2	11.1	Control 2 Parietal Ctx	33.9	36.9
Control 2 Temporal Ctx	43.2	39.8	Control 3 Parietal Ctx	33.0	28.7
Control 3 Temporal Ctx	16.7	18.3	Control (Path) 1 Parietal Ctx	63.7	67.8
Control 4 Temporal Ctx	18.3	19.8	Control (Path) 2 Parietal Ctx	30.6	30.4
Control (Path) 1 Temporal Ctx	51.4	48.0	Control (Path) 3 Parietal Ctx	8.1	9.7
Control (Path) 2 Temporal Ctx	39.2	45.7	Control (Path) 4	64.2	59.5

		Parietal Ctx	
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Table CRC. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3273, Run 215775405	Tissue Name	Rel. Exp.(%) Ag3273, Run 215775405
Adipose	7.1	Renal ca. TK-10	4.9
Melanoma* Hs688(A).T	0.0	Bladder	0.9
Melanoma* Hs688(B).T	0.0	Gastric ca. (liver met.) NCI-N87	2.4
Melanoma* M14	17.6	Gastric ca. KATO III	0.0
Melanoma* LOXIMVI	0.9	Colon ca. SW-948	0.0
Melanoma* SK- MEL-5	4.2	Colon ca. SW480	2.7
Squamous cell carcinoma SCC-4	0.2	Colon ca. * (SW480 met) SW620	1.0
Testis Pool	13.5	Colon ca. HT29	0.1
Prostate ca.* (bone met) PC-3	2.7	Colon ca. HCT-116	6.0
Prostate Pool	0.2	Colon ca. CaCo-2	2.0
Placenta	0.0	Colon cancer tissue	0.6
Uterus Pool	0.0	Colon ca. SW1116	0.4
Ovarian ca. OVCAR-3	5.4	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV- 3	6.8	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	1.6	Colon Pool	0.4
Ovarian ca. OVCAR-5	2.1	Small Intestine Pool	0.1
Ovarian ca. IGROV- 1	7.7	Stomach Pool	0.3
Ovarian ca. OVCAR-8	9.6	Bone Marrow Pool	0.1
Ovary	0.8	Fetal Heart	100.0
Breast ca. MCF-7	1.7	Heart Pool	0.2
Breast ca. MDA- MB-231	0.8	Lymph Node Pool	0.0
Breast ca. BT 549	7.7	Fetal Skeletal Muscle	0.3
Breast ca. T47D	9.3	Skeletal Muscle Pool	1.3
Breast ca. MDA-N	0.0	Spleen Pool	0.0
Breast Pool	0.4	Thymus Pool	0.4

Trachea	0.2	CNS cancer (glio/astro) U87-MG	0.0
Lung	0.0	CNS cancer (glio/astro) U-118-MG	0.0
Fetal Lung	0.3	CNS cancer (neuro;met) SK-N-AS	0.0
Lung ca. NCI-N417	5.1	CNS cancer (astro) SF- 539	0.2
Lung ca. LX-1	0.4	CNS cancer (astro) SNB-75	0.6
Lung ca. NCI-H146	12.2	CNS cancer (glio) SNB-19	7.1
Lung ca. SHP-77	2.4	CNS cancer (glio) SF- 295	1.8
Lung ca. A549	3.4	Brain (Amygdala) Pool	31.4
Lung ca. NCI-H526	12.0	Brain (cerebellum)	32.3
Lung ca. NCI-H23	5.8	Brain (fetal)	9.3
Lung ca. NCI-H460	2.3	Brain (Hippocampus) Pool	22.5
Lung ca. HOP-62	1.0	Cerebral Cortex Pool	40.3
Lung ca. NCI-H522	7.4	Brain (Substantia nigra) Pool	57.4
Liver	0.0	Brain (Thalamus) Pool	36.6
Fetal Liver	0.1	Brain (whole)	24.8
Liver ca. HepG2	0.3	Spinal Cord Pool	20.2
Kidney Pool	0.2	Adrenal Gland	0.0
Fetal Kidney	0.7	Pituitary gland Pool	2.2
Renal ca. 786-0	0.2	Salivary Gland	0.2
Renal ca. A498	1.0	Thyroid (female)	1.1
Renal ca. ACHN	4.5	Pancreatic ca. CAPAN2	0.0
Renal ca. UO-31	3.7	Pancreas Pool	0.6

Table CRD. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3273, Run 165338992	Tissue Name	Rel. Exp.(%) Ag3273, Run 165338992
Secondary Th1 act	1.0	HUVEC IL-1beta	0.0
Secondary Th2 act	2.5	HUVEC IFN gamma	0.0
Secondary Tr1 act	3.7	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	5.0	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	0.9	HUVEC IL-11	0.0
Secondary Tr1 rest	6.9	Lung Microvascular EC	0.0

		none	
Primary Th1 act	6.2	Lung Microvascular EC TNFalpha + IL-1beta	0.0
Primary Th2 act	5.9	Microvascular Dermal EC none	0.0
Primary Tr1 act	9.5	Microvascular Dermal EC TNFalpha + IL-1beta	0.0
Primary Th1 rest	3.1	Bronchial epithelium TNFalpha + IL1beta	0.0
Primary Th2 rest	0.0	Small airway epithelium none	2.9
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	0.0
CD45RA CD4 lymphocyte act	0.0	Coronary artery SMC rest	1.8
CD45RO CD4 lymphocyte act	0.0	Coronary artery SMC TNFalpha + IL-1beta	0.0
CD8 lymphocyte act	0.0	Astrocytes rest	16.5
Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFalpha + IL-1beta	10.4
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	0.0
2ry Th1/Th2/Tr1_anti- CD95 CH11	19.1	CCD1106 (Keratinocytes) none	0.0
LAK cells rest	0.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0
LAK cells IL-2	1.2	Liver cirrhosis	12.7
LAK cells IL-2+IL-12	2.5	Lupus kidney	3.9
LAK cells IL-2+IFN gamma	4.1	NCI-H292 none	10.8
LAK cells IL-2+ IL-18	0.0	NCI-H292 IL-4	23.2
LAK cells PMA/ionomycin	0.0	NCI-H292 IL-9	22.4
NK Cells IL-2 rest	0.0	NCI-H292 IL-13	10.3
Two Way MLR 3 day	1.1	NCI-H292 IFN gamma	18.0
Two Way MLR 5 day	0.0	HPAEC none	0.0
Two Way MLR 7 day	0.0	HPAEC TNF alpha + IL-1 beta	0.0
PBMC rest	0.0	Lung fibroblast none	1.9
PBMC PWM	1.2	Lung fibroblast TNF alpha + IL-1 beta	0.0
PBMC PHA-L	0.0	Lung fibroblast IL-4	3.8
Ramos (B cell) none	0.0	Lung fibroblast IL-9	0.5

Ramos (B cell) ionomycin	0.0	Lung fibroblast IL-13	5.7
B lymphocytes PWM	3.5	Lung fibroblast IFN gamma	2.9
B lymphocytes CD40L and IL-4	0.0	Dermal fibroblast CCD1070 rest	0.0
EOL-1 dbcAMP	100.0	Dermal fibroblast CCD1070 TNF alpha	0.0
EOL-1 dbcAMP PMA/ionomycin	25.9	Dermal fibroblast CCD1070 IL-1 beta	0.0
Dendritic cells none	3.8	Dermal fibroblast IFN gamma	2.8
Dendritic cells LPS	2.6	Dermal fibroblast IL-4	4.8
Dendritic cells anti-CD40	5.0	IBD Colitis 2	0.0
Monocytes rest	0.0	IBD Crohn's	0.0
Monocytes LPS	0.0	Colon	37.4
Macrophages rest	4.2	Lung	8.4
Macrophages LPS	0.0	Thymus	40.9
HUVEC none	0.0	Kidney	6.3
HUVEC starved	0.0		

CNS_neurodegeneration_v1.0 Summary: Ag3273 Two experiments with the same probe and primer set produce results that are in excellent agreement. This panel confirms the expression of this gene at low to moderate levels in the brains of an independent group of individuals. Expression of this gene is found to be down-regulated in the temporal cortex of Alzheimer's disease patients. Therefore, up-regulation of this gene or its protein product, or treatment with specific agonists for this protein, may be of use in reversing the dementia/memory loss associated with Alzheimer's disease and neuronal death.

General_screening_panel_v1.4 Summary: Ag3273 Highest expression of the CG57460-01 gene is seen in fetal heart (CT=28.6). In addition, this gene is expressed at much higher levels in fetal heart when compared to expression in the adult heart (CT=38). Thus, expression of this gene may be used to differentiate between the fetal and adult source of this tissue. In addition, the higher expression in fetal heart suggests that this protein product may be involved in the development of this organ. Therefore, therapeutic modulation of the expression or function of this gene may be useful in the treatment of heart disease.

This gene also shows highly specific brain expression. Please see Panel CNS_neurodegeneration for discussion of utility of this gene in the central nervous system.

In addition, expression of this gene appears to be upregulated in a number of cancer cell lines when compared to the normal tissues. Specifically, expression of this gene appears to be higher in ovarian, breast, lung and renal cancer cell lines when compared to their respective normal tissues. Therefore, therapeutic modulation of the activity of this gene or its protein may be of benefit in the treatment of ovarian, breast, lung and renal cancer. The CG57460-01 gene encodes a transmembrane protein with homology to N-acetyltransferase Camello 2, a protein involved in cellular adhesion (ref. 1).

References:

1. Popsueva AE, Luchinskaya NN, Ludwig AV, Zinovjeva OY, Poteryaev DA, Feigelman MM, Ponomarev MB, Berekelya L, Belyavsky AV. Overexpression of camello, a member of a novel protein family, reduces blastomere adhesion and inhibits gastrulation in *Xenopus laevis*. Dev Biol 2001 Jun 15;234(2):483-96

Panel 4D Summary: Ag3273 Highest expression of the CG57460-01 is seen in eosinophils. In addition, differential expression is observed in the eosinophil cell line EOL-1 under resting conditions over that in EOL-1 cells stimulated by phorbol ester and ionomycin. Thus, this gene may be involved in eosinophil function. Therefore, therapeutic modulation of the expression or function of this gene may reduce eosinophil activation and be useful in the treatment of asthma and allergies.

In addition, significant expression in normal colon and thymus suggest a role for this gene in the normal homeostasis of these tissues. Therefore, therapeutic modulation of the expression or function of this gene may modulate immune function (T cell development) and be important for organ transplant, AIDS treatment or post chemotherapy immune reconstitution. Furthermore, since expression of this gene is decreased in colon samples from patients with IBD colitis and Crohn's disease relative to normal colon, therapeutic modulation of the activity of the protein encoded by this gene may be useful in the treatment of inflammatory bowel disease.

CS. CG57464-01

Expression of gene CG57464-01 was assessed using the primer-probe set Ag3248, described in Table CSA. Results of the RTQ-PCR runs are shown in Tables CSB, CSC, CSD and CSE.

Table CSA. Probe Name Ag3248

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-cctccctggtagaggtcaac-3'	20	929	695
Probe	TET-5'-ctactcagtgccagcagccaggt-3'- TAMRA	24	954	696
Reverse	5'-tgtctgcatgcagcctatg-3'	19	996	697

Table CSB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3248, Run 210037962	Rel. Exp.(%) Ag3248, Run 224063124	Tissue Name	Rel. Exp.(%) Ag3248, Run 210037962	Rel. Exp.(%) Ag3248, Run 224063124
AD 1 Hippo	26.4	4.8	Control (Path) 3 Temporal Ctx	28.5	39.2
AD 2 Hippo	73.2	71.7	Control (Path) 4 Temporal Ctx	57.8	61.1
AD 3 Hippo	21.6	5.6	AD 1 Occipital Ctx	19.1	21.2
AD 4 Hippo	28.3	28.9	AD 2 Occipital Ctx (Missing)	0.0	0.0
AD 5 hippo	85.3	100.0	AD 3 Occipital Ctx	13.0	15.9
AD 6 Hippo	70.2	72.7	AD 4 Occipital Ctx	37.4	28.7
Control 2 Hippo	64.6	49.3	AD 5 Occipital Ctx	33.9	85.3
Control 4 Hippo	55.5	64.2	AD 6 Occipital Ctx	58.6	14.4
Control (Path) 3 Hippo	46.3	0.9	Control 1 Occipital Ctx	17.3	22.7
AD 1 Temporal Ctx	28.9	24.1	Control 2 Occipital Ctx	89.5	81.2

AD 2 Temporal Ctx	57.4	62.4	Control 3 Occipital Ctx	68.3	62.0
AD 3 Temporal Ctx	18.9	16.7	Control 4 Occipital Ctx	29.3	34.2
AD 4 Temporal Ctx	42.3	29.9	Control (Path) 1 Occipital Ctx	100.0	92.7
AD 5 Inf Temporal Ctx	77.4	97.3	Control (Path) 2 Occipital Ctx	36.3	15.1
AD 5 Sup Temporal Ctx	69.7	87.7	Control (Path) 3 Occipital Ctx	32.5	25.2
AD 6 Inf Temporal Ctx	39.2	87.1	Control (Path) 4 Occipital Ctx	70.2	66.9
AD 6 Sup Temporal Ctx	73.2	70.7	Control 1 Parietal Ctx	24.8	32.3
Control 1 Temporal Ctx	25.3	26.1	Control 2 Parietal Ctx	70.7	94.0
Control 2 Temporal Ctx	43.5	77.4	Control 3 Parietal Ctx	59.0	0.0
Control 3 Temporal Ctx	74.2	49.3	Control (Path) 1 Parietal Ctx	42.6	80.7
Control 4 Temporal Ctx	45.7	68.8	Control (Path) 2 Parietal Ctx	67.4	59.9
Control (Path) 1 Temporal Ctx	63.3	58.6	Control (Path) 3 Parietal Ctx	25.3	24.1
Control (Path) 2 Temporal Ctx	55.9	55.1	Control (Path) 4 Parietal Ctx	78.5	79.0

Table CSC. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3248, Run 214693634	Tissue Name	Rel. Exp.(%) Ag3248, Run 214693634
Adipose	1.5	Renal ca. TK-10	3.6
Melanoma*	6.2	Bladder	7.6

Hs688(A).T			
Melanoma* Hs688(B).T	5.8	Gastric ca. (liver met.) NCI-N87	16.8
Melanoma* M14	4.9	Gastric ca. KATO III	14.5
Melanoma* LOXIMVI	5.3	Colon ca. SW-948	6.4
Melanoma* SK- MEL-5	4.3	Colon ca. SW480	15.6
Squamous cell carcinoma SCC-4	3.3	Colon ca.* (SW480 met) SW620	9.1
Testis Pool	1.5	Colon ca. HT29	7.1
Prostate ca.* (bone met) PC-3	2.3	Colon ca. HCT-116	7.5
Prostate Pool	3.1	Colon ca. CaCo-2	8.7
Placenta	3.0	Colon cancer tissue	4.9
Uterus Pool	0.9	Colon ca. SW1116	10.2
Ovarian ca. OVCAR-3	24.0	Colon ca. Colo-205	6.2
Ovarian ca. SK-OV- 3	18.7	Colon ca. SW-48	7.5
Ovarian ca. OVCAR-4	4.1	Colon Pool	4.2
Ovarian ca. OVCAR-5	33.0	Small Intestine Pool	4.5
Ovarian ca. IGROV- 1	16.0	Stomach Pool	2.7
Ovarian ca. OVCAR-8	20.9	Bone Marrow Pool	1.3
Ovary	3.1	Fetal Heart	3.2
Breast ca. MCF-7	4.5	Heart Pool	2.6
Breast ca. MDA- MB-231	12.2	Lymph Node Pool	4.6
Breast ca. BT 549	12.0	Fetal Skeletal Muscle	1.2
Breast ca. T47D	100.0	Skeletal Muscle Pool	4.0
Breast ca. MDA-N	9.7	Spleen Pool	4.1
Breast Pool	5.2	Thymus Pool	5.3
Trachea	3.1	CNS cancer (glio/astro) U87-MG	12.1
Lung	0.4	CNS cancer (glio/astro) U-118-MG	10.9
Fetal Lung	4.4	CNS cancer (neuro;met) SK-N-AS	16.0
Lung ca. NCI-N417	3.1	CNS cancer (astro) SF- 539	6.2

Lung ca. LX-1	12.5	CNS cancer (astro) SNB-75	15.3
Lung ca. NCI-H146	5.1	CNS cancer (glio) SNB-19	13.2
Lung ca. SHP-77	1.5	CNS cancer (glio) SF- 295	25.9
Lung ca. A549	5.4	Brain (Amygdala) Pool	4.7
Lung ca. NCI-H526	7.4	Brain (cerebellum)	8.5
Lung ca. NCI-H23	4.4	Brain (fetal)	2.1
Lung ca. NCI-H460	4.5	Brain (Hippocampus) Pool	6.1
Lung ca. HOP-62	6.3	Cerebral Cortex Pool	6.0
Lung ca. NCI-H522	5.5	Brain (Substantia nigra) Pool	8.1
Liver	3.2	Brain (Thalamus) Pool	7.8
Fetal Liver	2.3	Brain (whole)	3.4
Liver ca. HepG2	5.4	Spinal Cord Pool	6.6
Kidney Pool	4.5	Adrenal Gland	3.0
Fetal Kidney	3.1	Pituitary gland Pool	3.4
Renal ca. 786-0	7.4	Salivary Gland	4.3
Renal ca. A498	5.8	Thyroid (female)	6.1
Renal ca. ACHN	5.6	Pancreatic ca. CAPAN2	11.3
Renal ca. UO-31	6.1	Pancreas Pool	5.2

Table CSD. Panel 2.2

Tissue Name	Rel. Exp.(%) Ag3248, Run 174441298	Tissue Name	Rel. Exp.(%) Ag3248, Run 174441298
Normal Colon	14.4	Kidney Margin (OD04348)	100.0
Colon cancer (OD06064)	6.3	Kidney malignant cancer (OD06204B)	6.3
Colon Margin (OD06064)	7.5	Kidney normal adjacent tissue (OD06204E)	9.3
Colon cancer (OD06159)	8.0	Kidney Cancer (OD04450-01)	57.8
Colon Margin (OD06159)	5.3	Kidney Margin (OD04450-03)	16.2
Colon cancer (OD06297-04)	2.4	Kidney Cancer 8120613	10.8
Colon Margin (OD06297-05)	6.3	Kidney Margin 8120614	16.7
CC Gr.2 ascend colon	14.1	Kidney Cancer 9010320	9.0

(ODO3921)			
CC Margin (ODO3921)	12.8	Kidney Margin 9010321	19.5
Colon cancer metastasis (OD06104)	4.4	Kidney Cancer 8120607	34.2
Lung Margin (OD06104)	4.8	Kidney Margin 8120608	27.7
Colon mets to lung (OD04451-01)	15.0	Normal Uterus	3.8
Lung Margin (OD04451-02)	6.7	Uterine Cancer 064011	10.5
Normal Prostate	9.0	Normal Thyroid	4.6
Prostate Cancer (OD04410)	7.5	Thyroid Cancer 064010	18.6
Prostate Margin (OD04410)	11.6	Thyroid Cancer A302152	24.0
Normal Ovary	28.7	Thyroid Margin A302153	13.3
Ovarian cancer (OD06283-03)	3.1	Normal Breast	4.0
Ovarian Margin (OD06283-07)	1.1	Breast Cancer (OD04566)	9.3
Ovarian Cancer 064008	6.8	Breast Cancer 1024	6.9
Ovarian cancer (OD06145)	8.6	Breast Cancer (OD04590-01)	86.5
Ovarian Margin (OD06145)	17.8	Breast Cancer Mets (OD04590-03)	22.4
Ovarian cancer (OD06455-03)	2.0	Breast Cancer Metastasis (OD04655- 05)	47.3
Ovarian Margin (OD06455-07)	2.5	Breast Cancer 064006	9.8
Normal Lung	4.7	Breast Cancer 9100266	5.8
Invasive poor diff. lung adeno (ODO4945-01)	9.0	Breast Margin 9100265	3.3
Lung Margin (ODO4945-03)	4.5	Breast Cancer A209073	7.3
Lung Malignant Cancer (OD03126)	10.6	Breast Margin A2090734	17.0
Lung Margin (OD03126)	8.4	Breast cancer (OD06083)	8.6
Lung Cancer (OD05014A)	8.7	Breast cancer node metastasis (OD06083)	8.2
Lung Margin (OD05014B)	8.6	Normal Liver	33.4

Lung cancer (OD06081)	6.3	Liver Cancer 1026	20.6
Lung Margin (OD06081)	4.4	Liver Cancer 1025	29.1
Lung Cancer (OD04237-01)	2.7	Liver Cancer 6004-T	27.4
Lung Margin (OD04237-02)	16.7	Liver Tissue 6004-N	2.5
Ocular Melanoma Metastasis	25.0	Liver Cancer 6005-T	26.2
Ocular Melanoma Margin (Liver)	15.8	Liver Tissue 6005-N	58.2
Melanoma Metastasis	3.8	Liver Cancer 064003	52.5
Melanoma Margin (Lung)	2.6	Normal Bladder	10.7
Normal Kidney	12.4	Bladder Cancer 1023	6.8
Kidney Ca, Nuclear grade 2 (OD04338)	32.3	Bladder Cancer A302173	3.8
Kidney Margin (OD04338)	7.1	Normal Stomach	16.8
Kidney Ca Nuclear grade 1/2 (OD04339)	71.7	Gastric Cancer 9060397	9.2
Kidney Margin (OD04339)	14.6	Stomach Margin 9060396	10.4
Kidney Ca, Clear cell type (OD04340)	8.4	Gastric Cancer 9060395	1.7
Kidney Margin (OD04340)	31.2	Stomach Margin 9060394	7.5
Kidney Ca, Nuclear grade 3 (OD04348)	7.5	Gastric Cancer 064005	10.7

Table CSE. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3248, Run 164390952	Tissue Name	Rel. Exp.(%) Ag3248, Run 164390952
Secondary Th1 act	15.3	HUVEC IL-1beta	1.7
Secondary Th2 act	16.5	HUVEC IFN gamma	16.0
Secondary Tr1 act	15.5	HUVEC TNF alpha + IFN gamma	7.8
Secondary Th1 rest	8.0	HUVEC TNF alpha + IL4	9.2
Secondary Th2 rest	8.8	HUVEC IL-11	12.8
Secondary Tr1 rest	12.8	Lung Microvascular EC none	19.1
Primary Th1 act	8.4	Lung Microvascular EC TNFalpha + IL-1beta	13.8

Primary Th2 act	9.3	Microvascular Dermal EC none	18.0
Primary Tr1 act	15.1	Microvascular Dermal EC TNFalpha + IL-1beta	6.9
Primary Th1 rest	12.3	Bronchial epithelium TNFalpha + IL1beta	21.3
Primary Th2 rest	4.6	Small airway epithelium none	13.5
Primary Tr1 rest	5.6	Small airway epithelium TNFalpha + IL-1beta	45.4
CD45RA CD4 lymphocyte act	12.1	Coronary artery SMC rest	12.9
CD45RO CD4 lymphocyte act	12.0	Coronary artery SMC TNFalpha + IL-1beta	15.2
CD8 lymphocyte act	12.5	Astrocytes rest	18.6
Secondary CD8 lymphocyte rest	13.7	Astrocytes TNFalpha + IL-1beta	17.2
Secondary CD8 lymphocyte act	9.9	KU-812 (Basophil) rest	8.7
CD4 lymphocyte none	6.8	KU-812 (Basophil) PMA/ionomycin	8.6
2ry Th1/Th2/Tr1 _anti-CD95 CH11	9.5	CCD1106 (Keratinocytes) none	10.9
LAK cells rest	15.2	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	12.2
LAK cells IL-2	13.6	Liver cirrhosis	7.4
LAK cells IL-2+IL-12	9.1	Lupus kidney	10.7
LAK cells IL-2+IFN gamma	13.9	NCI-H292 none	42.6
LAK cells IL-2+ IL-18	9.7	NCI-H292 IL-4	48.3
LAK cells PMA/ionomycin	1.5	NCI-H292 IL-9	54.3
NK Cells IL-2 rest	12.9	NCI-H292 IL-13	37.1
Two Way MLR 3 day	19.8	NCI-H292 IFN gamma	48.3
Two Way MLR 5 day	6.3	HPAEC none	17.9
Two Way MLR 7 day	9.7	HPAEC TNF alpha + IL-1 beta	5.0
PBMC rest	10.7	Lung fibroblast none	21.5
PBMC PWM	27.0	Lung fibroblast TNF alpha + IL-1 beta	27.9
PBMC PHA-L	12.0	Lung fibroblast IL-4	31.9
Ramos (B cell) none	27.9	Lung fibroblast IL-9	35.4
Ramos (B cell) ionomycin	100.0	Lung fibroblast IL-13	18.6
B lymphocytes PWM	21.0	Lung fibroblast IFN	37.4

		gamma	
B lymphocytes CD40L and IL-4	8.9	Dermal fibroblast CCD1070 rest	17.7
EOL-1 dbcAMP	19.8	Dermal fibroblast CCD1070 TNF alpha	21.2
EOL-1 dbcAMP PMA/ionomycin	1.4	Dermal fibroblast CCD1070 IL-1 beta	8.4
Dendritic cells none	18.3	Dermal fibroblast IFN gamma	16.8
Dendritic cells LPS	20.0	Dermal fibroblast IL-4	27.7
Dendritic cells anti-CD40	22.1	IBD Colitis 2	3.0
Monocytes rest	12.6	IBD Crohn's	4.2
Monocytes LPS	2.6	Colon	28.5
Macrophages rest	20.6	Lung	12.0
Macrophages LPS	10.4	Thymus	53.6
HUVEC none	11.9	Kidney	20.0
HUVEC starved	15.6		

CNS_neurodegeneration_v1.0 Summary: Ag3248 Results from two experiments using the same probe/primer set gave results that are in excellent agreement. This panel confirms the expression of this gene at low levels in the brains of an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. Please see Panel 1.4 for a discussion of the potential utility of this gene in treatment of central nervous system disorders.

General_screening_panel_v1.4 Summary: Ag3248 Expression of the CG57464-01 gene is highest in a breast cancer cell line (CT = 27). This also gene appears to be overexpressed in ovarian and CNS cancer cell lines when compared to the normal tissue controls. Thus, therapeutic modulation of the activity of this gene or its protein may be of benefit in the treatment of breast, ovarian and CNS cancer.

In addition, this gene is expressed at low levels in all regions of the central nervous system examined, including amygdala, hippocampus, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord. Therefore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

Among tissues with metabolic or endocrine function, this gene is expressed at low levels in pancreas, adipose, adrenal gland, thyroid, pituitary gland, skeletal muscle, heart, liver and the gastrointestinal tract. Therefore, therapeutic modulation of the activity of this gene may prove useful in the treatment of endocrine/metabolically related diseases, such as obesity and diabetes.

Panel 2.2 Summary: Ag3248 This gene is expressed at low to moderate levels in the majority of samples on this panel, with highest expression detected in a sample derived from normal kidney (CT = 28.6). Expression of the CG57464-01 gene appears to be upregulated in a number of breast cancer samples when compared to normal breast. Thus, therapeutic modulation of the activity of this gene or its protein product may be of benefit in the treatment of breast cancer.

Panel 4D Summary: Ag3248 Expression of the CG57464-01 gene is highest in Ramos B cells treated with ionomycin (CT = 29). Therefore, expression of this gene may be used as a marker of activated B cells. In addition, this gene is expressed at relatively high levels in lung fibroblasts as well as in the mucoepidermoid cell line NCI-H292 independent of treatment (CTs = 30), suggesting that therapeutic modulation of the activity of this gene or its protein product may be of benefit in the treatment of asthma and emphysema.

This gene is also expressed at low to moderate levels in a wide range of other cell types of significance in the immune response in health and disease. These cells include members of the T-cell, B-cell, endothelial cell, macrophage/monocyte, and peripheral blood mononuclear cell family, as well as epithelial and fibroblast cell types from lung and skin, and normal tissues represented by colon, lung, thymus and kidney. This ubiquitous pattern of expression suggests that this gene product may be involved in homeostatic processes for these and other cell types and tissues.

This pattern is in agreement with the expression profile in General_screening_panel_v1.5 and also suggests a role for the gene product in cell survival and proliferation.

Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma,

allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

CT. CG57466-01: Acetylglucosaminyltransferase

Expression of gene CG57466-01 was assessed using the primer-probe set Ag3249, described in Table CTA. Results of the RTQ-PCR runs are shown in Tables CTB, CTC and CTD.

Table CTA. Probe Name Ag3249

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-accactaactgctcagccaata-3'	22	156	698
Probe	TET-5'-aacttgaccaccagccctgggt-3'- TAMRA	23	180	699
Reverse	5'-tagaagagaaactgccggaact-3'	22	220	700

Table CTB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3249, Run 210037963	Tissue Name	Rel. Exp.(%) Ag3249, Run 210037963
AD 1 Hippo	8.4	Control (Path) 3 Temporal Ctx	5.6
AD 2 Hippo	41.5	Control (Path) 4 Temporal Ctx	27.2
AD 3 Hippo	14.0	AD 1 Occipital Ctx	6.6
AD 4 Hippo	26.1	AD 2 Occipital Ctx (Missing)	0.0
AD 5 Hippo	29.9	AD 3 Occipital Ctx	8.5
AD 6 Hippo	100.0	AD 4 Occipital Ctx	25.2
Control 2 Hippo	42.0	AD 5 Occipital Ctx	48.0
Control 4 Hippo	29.3	AD 6 Occipital Ctx	22.4
Control (Path) 3 Hippo	5.6	Control 1 Occipital Ctx	6.1
AD 1 Temporal Ctx	10.7	Control 2 Occipital Ctx	51.4
AD 2 Temporal Ctx	25.5	Control 3 Occipital Ctx	22.1
AD 3 Temporal Ctx	9.9	Control 4 Occipital Ctx	15.8
AD 4 Temporal Ctx	29.9	Control (Path) 1 Occipital Ctx	92.7

AD 5 Inf Temporal Ctx	25.5	Control (Path) 2 Occipital Ctx	18.7
AD 5 Sup Temporal Ctx	27.4	Control (Path) 3 Occipital Ctx	0.7
AD 6 Inf Temporal Ctx	87.1	Control (Path) 4 Occipital Ctx	29.9
AD 6 Sup Temporal Ctx	5.0	Control 1 Parietal Ctx	13.7
Control 1 Temporal Ctx	24.5	Control 2 Parietal Ctx	29.1
Control 2 Temporal Ctx	41.2	Control 3 Parietal Ctx	25.7
Control 3 Temporal Ctx	33.7	Control (Path) 1 Parietal Ctx	64.2
Control 3 Temporal Ctx	21.9	Control (Path) 2 Parietal Ctx	25.9
Control (Path) 1 Temporal Ctx	69.7	Control (Path) 3 Parietal Ctx	1.9
Control (Path) 2 Temporal Ctx	26.4	Control (Path) 4 Parietal Ctx	39.8

Table CTC. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3249, Run 214693635	Tissue Name	Rel. Exp.(%) Ag3249, Run 214693635
Adipose	5.6	Renal ca. TK-10	2.7
Melanoma* Hs688(A).T	0.4	Bladder	59.5
Melanoma* Hs688(B).T	0.5	Gastric ca. (liver met.) NCI-N87	78.5
Melanoma* M14	8.8	Gastric ca. KATO III	60.3
Melanoma* LOXIMVI	0.1	Colon ca. SW-948	0.5
Melanoma* SK-MEL-5	15.2	Colon ca. SW480	4.4
Squamous cell carcinoma SCC-4	50.7	Colon ca.* (SW480 met) SW620	0.9
Testis Pool	1.7	Colon ca. HT29	0.8
Prostate ca.* (bone met) PC-3	9.0	Colon ca. HCT-116	13.2
Prostate Pool	1.8	Colon ca. CaCo-2	6.6
Placenta	10.9	Colon cancer tissue	26.6
Uterus Pool	0.9	Colon ca. SW1116	3.6
Ovarian ca. OVCAR-3	3.8	Colon ca. Colo-205	0.1

Ovarian ca. SK-OV-3	6.1	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	1.3	Colon Pool	6.2
Ovarian ca. OVCAR-5	22.1	Small Intestine Pool	11.3
Ovarian ca. IGROV-1	7.5	Stomach Pool	6.7
Ovarian ca. OVCAR-8	1.4	Bone Marrow Pool	2.3
Ovary	24.5	Fetal Heart	11.6
Breast ca. MCF-7	0.7	Heart Pool	2.7
Breast ca. MDA-MB-231	1.4	Lymph Node Pool	7.1
Breast ca. BT 549	1.8	Fetal Skeletal Muscle	0.4
Breast ca. T47D	37.9	Skeletal Muscle Pool	0.8
Breast ca. MDA-N	100.0	Spleen Pool	13.3
Breast Pool	4.0	Thymus Pool	3.7
Trachea	65.5	CNS cancer (glio/astro) U87-MG	0.0
Lung	5.8	CNS cancer (glio/astro) U-118-MG	0.7
Fetal Lung	87.7	CNS cancer (neuro;met) SK-N-AS	21.3
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF-539	0.1
Lung ca. LX-1	29.5	CNS cancer (astro) SNB-75	12.2
Lung ca. NCI-H146	0.6	CNS cancer (glio) SNB-19	6.5
Lung ca. SHP-77	0.2	CNS cancer (glio) SF-295	6.2
Lung ca. A549	12.9	Brain (Amygdala) Pool	5.1
Lung ca. NCI-H526	0.0	Brain (cerebellum)	6.8
Lung ca. NCI-H23	2.3	Brain (fetal)	4.5
Lung ca. NCI-H460	0.2	Brain (Hippocampus) Pool	6.7
Lung ca. HOP-62	5.0	Cerebral Cortex Pool	6.7
Lung ca. NCI-H522	0.4	Brain (Substantia nigra) Pool	7.6
Liver	0.8	Brain (Thalamus) Pool	9.0
Fetal Liver	4.8	Brain (whole)	7.5
Liver ca. HepG2	0.0	Spinal Cord Pool	4.6
Kidney Pool	11.7	Adrenal Gland	40.6

Fetal Kidney	4.5	Pituitary gland Pool	10.5
Renal ca. 786-0	2.5	Salivary Gland	5.7
Renal ca. A498	1.4	Thyroid (female)	5.8
Renal ca. ACHN	22.2	Pancreatic ca. CAPAN2	43.8
Renal ca. UO-31	32.8	Pancreas Pool	11.3

Table CTD. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3249, Run 164390953	Tissue Name	Rel. Exp.(%) Ag3249, Run 164390953
Secondary Th1 act	0.2	HUVEC IL-1beta	0.4
Secondary Th2 act	0.0	HUVEC IFN gamma	1.0
Secondary Tr1 act	0.0	HUVEC TNF alpha + IFN gamma	0.5
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	0.6
Secondary Th2 rest	0.1	HUVEC IL-11	0.9
Secondary Tr1 rest	0.0	Lung Microvascular EC none	1.4
Primary Th1 act	0.2	Lung Microvascular EC TNFalpha + IL-1beta	4.5
Primary Th2 act	0.0	Microvascular Dermal EC none	0.9
Primary Tr1 act	0.0	Microvascular Dermal EC TNFalpha + IL-1beta	7.7
Primary Th1 rest	0.1	Bronchial epithelium TNFalpha + IL1beta	3.6
Primary Th2 rest	0.0	Small airway epithelium none	0.2
Primary Tr1 rest	0.1	Small airway epithelium TNFalpha + IL-1beta	5.8
CD45RA CD4 lymphocyte act	0.5	Coronary artery SMC rest	0.0
CD45RO CD4 lymphocyte act	0.1	Coronary artery SMC TNFalpha + IL-1beta	0.0
CD8 lymphocyte act	0.6	Astrocytes rest	0.8
Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFalpha + IL-1beta	3.1
Secondary CD8 lymphocyte act	0.1	KU-812 (Basophil) rest	2.7
CD4 lymphocyte none	1.1	KU-812 (Basophil) PMA/ionomycin	3.8
2ry Th1/Th2/Tr1_anti- CD95 CH11	0.1	CCD1106 (Keratinocytes) none	1.6

LAK cells rest	1.9	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	1.3
LAK cells IL-2	5.0	Liver cirrhosis	3.2
LAK cells IL-2+IL-12	1.6	Lupus kidney	1.3
LAK cells IL-2+IFN gamma	5.0	NCI-H292 none	100.0
LAK cells IL-2+ IL-18	4.3	NCI-H292 IL-4	87.7
LAK cells PMA/ionomycin	6.1	NCI-H292 IL-9	96.6
NK Cells IL-2 rest	12.7	NCI-H292 IL-13	54.0
Two Way MLR 3 day	0.6	NCI-H292 IFN gamma	25.2
Two Way MLR 5 day	1.6	HPAEC none	0.4
Two Way MLR 7 day	0.9	HPAEC TNF alpha + IL-1 beta	6.3
PBMC rest	9.4	Lung fibroblast none	0.1
PBMC PWM	3.7	Lung fibroblast TNF alpha + IL-1 beta	0.3
PBMC PHA-L	0.7	Lung fibroblast IL-4	0.7
Ramos (B cell) none	0.1	Lung fibroblast IL-9	0.0
Ramos (B cell) ionomycin	2.0	Lung fibroblast IL-13	0.3
B lymphocytes PWM	2.7	Lung fibroblast IFN gamma	0.4
B lymphocytes CD40L and IL-4	5.8	Dermal fibroblast CCD1070 rest	0.1
EOL-1 dbcAMP	26.6	Dermal fibroblast CCD1070 TNF alpha	0.8
EOL-1 dbcAMP PMA/ionomycin	8.4	Dermal fibroblast CCD1070 IL-1 beta	0.0
Dendritic cells none	3.2	Dermal fibroblast IFN gamma	0.0
Dendritic cells LPS	2.5	Dermal fibroblast IL-4	0.0
Dendritic cells anti- CD40	1.3	IBD Colitis 2	1.4
Monocytes rest	0.4	IBD Crohn's	4.2
Monocytes LPS	10.5	Colon	48.6
Macrophages rest	1.1	Lung	19.5
Macrophages LPS	17.9	Thymus	2.5
HUVEC none	0.8	Kidney	3.9
HUVEC starved	1.1		

CNS_neurodegeneration_v1.0 Summary: Ag3249 This panel confirms the expression of this gene at low levels in the brains of an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem

brains and those of non-demented controls in this experiment. Please see Panel 1.4 for a discussion of the potential utility of this gene in treatment of central nervous system disorders.

General_screening_panel_v1.4 Summary: Ag3249 The CG57466-01 gene encodes a protein with homology to beta-1,3-galactosyltransferases, which catalyze the formation of type I oligosaccharides (ref. 1). Expression of this gene is highest in a breast cancer cell line (CT = 28.1). In addition, expression of this gene appears to be upregulated in pancreatic and gastric cancer cell lines when compared to their respective normal tissues. Thus, therapeutic modulation of the activity of this gene or its protein product may be of benefit in the treatment of breast, pancreatic and gastric cancer.

This gene also shows significant levels of expression in trachea, bladder and fetal lung. Interestingly, CG57466-01 gene expression is much higher in fetal lung (CT = 28.3) than in adult lung (CT = 32.2), suggesting that expression of this gene can be used to distinguish adult from fetal lung.

In addition, this gene is expressed at low levels in all regions of the central nervous system examined, including amygdala, hippocampus, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord. Therefore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

Among tissues with metabolic or endocrine function, this gene is expressed at low to moderate levels in pancreas, adipose, adrenal gland, thyroid, pituitary gland, heart, fetal liver and the gastrointestinal tract. Therefore, therapeutic modulation of the activity of this gene may prove useful in the treatment of endocrine/metabolically related diseases, such as obesity and diabetes.

References:

1. Shiraishi N, Natsume A, Togayachi A, Endo T, Akashima T, Yamada Y, Imai N, Nakagawa S, Koizumi S, Sekine S, Narimatsu H, Sasaki K. Identification and characterization of three novel beta 1,3-N-acetylglucosaminyltransferases structurally related to the beta 1,3-galactosyltransferase family. J Biol Chem 2001 Feb 2;276(5):3498-507

Panel 4D Summary: Ag3249 This transcript is most highly expressed in a cluster of treated and untreated samples derived from the NCI-H292 cell line, a human airway epithelial cell line that produces mucins (CTs = 30-32). Mucus overproduction is an important feature of bronchial asthma and chronic obstructive pulmonary disease samples. The transcript is also expressed at lower but still significant levels in small airway epithelium treated with IL-1 beta and TNF-alpha. The expression of the transcript in this mucoepidermoid cell line that is often used as a model for airway epithelium (NCI-H292 cells) suggests that this transcript may be important in the proliferation or activation of airway epithelium. Therefore, therapeutics designed with the protein encoded by the transcript may reduce or eliminate symptoms caused by inflammation in lung epithelia in chronic obstructive pulmonary disease, asthma, allergy, and emphysema.

CU. CG57468-01: multidrug resistance protein 1

Expression of gene CG57468-01 was assessed using the primer-probe set Ag3250, described in Table CUA. Results of the RTQ-PCR runs are shown in Tables CUB.

Table CUA. Probe Name Ag3250

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-agcaggggaaattttaacgat-3'	21	2391	701
Probe	TET-5'-agacacttggccttcaaagccatggt-3'-TAMRA	26	2419	702
Reverse	5'-caaaccaggcaatatcctgata-3'	22	2446	703

Table CUB. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3250, Run 214693636	Tissue Name	Rel. Exp.(%) Ag3250, Run 214693636
Adipose	0.1	Renal ca. TK-10	0.0
Melanoma* Hs688(A).T	0.0	Bladder	0.0
Melanoma* Hs688(B).T	0.0	Gastric ca. (liver met.) NCI-N87	0.0
Melanoma* M14	0.0	Gastric ca. KATO III	0.0
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	11.9
Melanoma* SK-MEL-5	0.6	Colon ca. SW480	0.0
Squamous cell	0.0	Colon ca.* (SW480	0.0

carcinoma SCC-4		met) SW620	
Testis Pool	0.0	Colon ca. HT29	0.0
Prostate ca.* (bone met) PC-3	0.0	Colon ca. HCT-116	0.0
Prostate Pool	0.0	Colon ca. CaCo-2	0.0
Placenta	0.0	Colon cancer tissue	0.0
Uterus Pool	0.0	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	0.0	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV-3	0.0	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	0.0	Colon Pool	0.1
Ovarian ca. OVCAR-5	0.0	Small Intestine Pool	0.0
Ovarian ca. IGROV-1	0.0	Stomach Pool	0.0
Ovarian ca. OVCAR-8	0.0	Bone Marrow Pool	0.0
Ovary	0.0	Fetal Heart	0.0
Breast ca. MCF-7	0.0	Heart Pool	0.7
Breast ca. MDA-MB-231	0.0	Lymph Node Pool	0.8
Breast ca. BT 549	0.0	Fetal Skeletal Muscle	0.0
Breast ca. T47D	0.0	Skeletal Muscle Pool	0.0
Breast ca. MDA-N	0.3	Spleen Pool	0.0
Breast Pool	100.0	Thymus Pool	0.0
Trachea	0.0	CNS cancer (glio/astro) U87-MG	0.0
Lung	0.0	CNS cancer (glio/astro) U-118-MG	0.0
Fetal Lung	0.1	CNS cancer (neuro;met) SK-N-AS	0.0
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF-539	0.0
Lung ca. LX-1	0.0	CNS cancer (astro) SNB-75	0.0
Lung ca. NCI-H146	0.0	CNS cancer (glio) SNB-19	0.0
Lung ca. SHP-77	0.0	CNS cancer (glio) SF-295	0.0
Lung ca. A549	0.0	Brain (Amygdala) Pool	0.0
Lung ca. NCI-H526	0.0	Brain (cerebellum)	0.0
Lung ca. NCI-H23	0.0	Brain (fetal)	0.0

Lung ca. NCI-H460	0.0	Brain (Hippocampus) Pool	0.0
Lung ca. HOP-62	0.0	Cerebral Cortex Pool	0.0
Lung ca. NCI-H522	0.0	Brain (Substantia nigra) Pool	0.0
Liver	9.5	Brain (Thalamus) Pool	0.0
Fetal Liver	21.0	Brain (whole)	0.0
Liver ca. HepG2	0.0	Spinal Cord Pool	0.0
Kidney Pool	17.4	Adrenal Gland	0.0
Fetal Kidney	6.5	Pituitary gland Pool	0.0
Renal ca. 786-0	0.0	Salivary Gland	0.0
Renal ca. A498	0.0	Thyroid (female)	0.0
Renal ca. ACHN	0.0	Pancreatic ca. CAPAN2	0.0
Renal ca. UO-31	0.0	Pancreas Pool	0.0

CNS_neurodegeneration_v1.0 Summary: Ag3250 Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.4 Summary: Ag3250 Expression of the CG57468-01 gene is highest in normal breast (CT = 23.8). In addition, this gene is highly expressed in fetal/adult kidney and fetal/adult liver (CTs = 26-27). Thus, expression of this gene may be used to distinguish these tissues from the other samples on this panel. Strikingly, expression of this gene is much lower in breast, kidney, and liver cancer cell lines. Therapeutic modulation of the activity of this gene or its protein product may be of benefit in the treatment of these types of cancers.

Panel 4D Summary: Ag3250 Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

CV. CG59609-01: PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A

Expression of gene CG59609-01 was assessed using the primer-probe set Ag3494, described in Table CVA. Results of the RTQ-PCR runs are shown in Tables CVB and CVC.

Table CVA. Probe Name Ag3494

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-ccgttctatcagccatggt-3'	19	3	704
Probe	TET-5'-ccccaccaggttcttagacatcatcg-3'-TAMRA	26	25	705

Reverse	5'-aaggagacacgtcccaagag-3'	20	62	706
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Table CVB. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3494, Run 217215292	Tissue Name	Rel. Exp.(%) Ag3494, Run 217215292
Adipose	0.0	Renal ca. TK-10	0.0
Melanoma* Hs688(A).T	0.0	Bladder	0.0
Melanoma* Hs688(B).T	0.0	Gastric ca. (liver met.) NCI-N87	0.0
Melanoma* M14	25.5	Gastric ca. KATO III	0.0
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.0
Melanoma* SK- MEL-5	0.0	Colon ca. SW480	0.0
Squamous cell carcinoma SCC-4	33.4	Colon ca.* (SW480 met) SW620	0.0
Testis Pool	100.0	Colon ca. HT29	0.0
Prostate ca.* (bone met) PC-3	0.0	Colon ca. HCT-116	0.0
Prostate Pool	0.0	Colon ca. CaCo-2	0.0
Placenta	0.0	Colon cancer tissue	0.0
Uterus Pool	0.0	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	0.0	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV- 3	0.0	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	0.0	Colon Pool	0.0
Ovarian ca. OVCAR-5	0.0	Small Intestine Pool	0.0
Ovarian ca. IGROV- 1	79.0	Stomach Pool	0.0
Ovarian ca. OVCAR-8	0.0	Bone Marrow Pool	0.0
Ovary	0.0	Fetal Heart	0.0
Breast ca. MCF-7	0.0	Heart Pool	0.0
Breast ca. MDA- MB-231	41.8	Lymph Node Pool	0.0
Breast ca. BT 549	0.0	Fetal Skeletal Muscle	0.0
Breast ca. T47D	0.0	Skeletal Muscle Pool	0.0
Breast ca. MDA-N	86.5	Spleen Pool	0.0
Breast Pool	0.0	Thymus Pool	0.0

Trachea	0.0	CNS cancer (glio/astro) U87-MG	0.0
Lung	0.0	CNS cancer (glio/astro) U-118-MG	0.0
Fetal Lung	0.0	CNS cancer (neuro;met) SK-N-AS	0.0
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF- 539	0.0
Lung ca. LX-1	0.0	CNS cancer (astro) SNB-75	0.0
Lung ca. NCI-H146	0.0	CNS cancer (glio) SNB-19	0.0
Lung ca. SHP-77	40.6	CNS cancer (glio) SF- 295	0.0
Lung ca. A549	0.0	Brain (Amygdala) Pool	0.0
Lung ca. NCI-H526	0.0	Brain (cerebellum)	0.0
Lung ca. NCI-H23	0.0	Brain (fetal)	0.0
Lung ca. NCI-H460	0.0	Brain (Hippocampus) Pool	0.0
Lung ca. HOP-62	0.0	Cerebral Cortex Pool	0.0
Lung ca. NCI-H522	0.0	Brain (Substantia nigra) Pool	0.0
Liver	0.0	Brain (Thalamus) Pool	0.0
Fetal Liver	0.0	Brain (whole)	0.0
Liver ca. HepG2	0.0	Spinal Cord Pool	0.0
Kidney Pool	47.0	Adrenal Gland	0.0
Fetal Kidney	0.0	Pituitary gland Pool	0.0
Renal ca. 786-0	0.0	Salivary Gland	0.0
Renal ca. A498	0.0	Thyroid (female)	0.0
Renal ca. ACHN	0.0	Pancreatic ca. CAPAN2	0.0
Renal ca. UO-31	0.0	Pancreas Pool	0.0

Table CVC. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3494, Run 166441744	Tissue Name	Rel. Exp.(%) Ag3494, Run 166441744
Secondary Th1 act	0.0	HUVEC IL-1beta	0.0
Secondary Th2 act	0.0	HUVEC IFN gamma	0.0
Secondary Tr1 act	0.0	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	0.0	HUVEC IL-11	0.0
Secondary Tr1 rest	0.0	Lung Microvascular EC	0.0

		none	
Primary Th1 act	0.0	Lung Microvascular EC TNFalpha + IL-1beta	10.2
Primary Th2 act	0.0	Microvascular Dermal EC none	0.0
Primary Tr1 act	0.0	Microsvascular Dermal EC TNFalpha + IL-1beta	0.0
Primary Th1 rest	0.0	Bronchial epithelium TNFalpha + IL1beta	0.0
Primary Th2 rest	0.0	Small airway epithelium none	0.0
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	0.0
CD45RA CD4 lymphocyte act	0.0	Coronary artery SMC rest	0.0
CD45RO CD4 lymphocyte act	0.0	Coronary artery SMC TNFalpha + IL-1beta	0.0
CD8 lymphocyte act	0.0	Astrocytes rest	0.0
Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFalpha + IL-1beta	0.0
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	0.0
2ry Th1/Th2/Tr1_anti- CD95 CH11	0.0	CCD1106 (Keratinocytes) none	0.0
LAK cells rest	0.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0
LAK cells IL-2	0.0	Liver cirrhosis	100.0
LAK cells IL-2+IL-12	5.6	Lupus kidney	4.6
LAK cells IL-2+IFN gamma	0.0	NCI-H292 none	0.0
LAK cells IL-2+ IL-18	0.0	NCI-H292 IL-4	0.0
LAK cells PMA/ionomycin	0.0	NCI-H292 IL-9	0.0
NK Cells IL-2 rest	0.0	NCI-H292 IL-13	0.0
Two Way MLR 3 day	0.0	NCI-H292 IFN gamma	0.0
Two Way MLR 5 day	0.0	HPAEC none	0.0
Two Way MLR 7 day	0.0	HPAEC TNF alpha + IL-1 beta	0.0
PBMC rest	0.0	Lung fibroblast none	0.0
PBMC PWM	0.0	Lung fibroblast TNF alpha + IL-1 beta	0.0
PBMC PHA-L	0.0	Lung fibroblast IL-4	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-9	0.0

Ramos (B cell) ionomycin	0.0	Lung fibroblast IL-13	0.0
B lymphocytes PWM	0.0	Lung fibroblast IFN gamma	0.0
B lymphocytes CD40L and IL-4	0.0	Dermal fibroblast CCD1070 rest	7.7
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 TNF alpha	0.0
EOL-1 dbcAMP PMA/ionomycin	0.0	Dermal fibroblast CCD1070 IL-1 beta	1.4
Dendritic cells none	0.0	Dermal fibroblast IFN gamma	0.0
Dendritic cells LPS	0.0	Dermal fibroblast IL-4	0.0
Dendritic cells anti-CD40	0.0	IBD Colitis 2	26.2
Monocytes rest	0.0	IBD Crohn's	13.8
Monocytes LPS	0.0	Colon	17.6
Macrophages rest	0.0	Lung	8.1
Macrophages LPS	0.0	Thymus	16.5
HUVEC none	0.0	Kidney	0.0
HUVEC starved	0.0		

CNS_neurodegeneration_v1.0 Summary: Ag3494 Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.4 Summary: Ag3494 Expression of the CG59609-01 gene is highest in testis (CT = 34.3). In addition, low but significant expression of this gene is detected in a breast cancer cell line and an ovarian cancer cell line. Thus, expression of this gene may be used to distinguish these samples from the other samples on this panel. Furthermore, therapeutic modulation of the activity of this gene may be of benefit in the treatment of fertility, breast cancer, and ovarian cancer.

Panel 4D Summary: Ag3494 Expression of the CG59609-01 gene is highest in a liver cirrhosis sample (CT = 34.3). In addition, low but significant expression of this gene is detected in samples from thymus as well as from normal and IBD colon. Thus, expression of this gene may be used to distinguish these samples from the other samples on this panel. Furthermore, therapies designed with the protein encoded for by this gene may potentially modulate liver function and play a role in the identification and treatment of inflammatory or autoimmune diseases which effect the liver including liver cirrhosis and fibrosis.

CW. CG59613-01: PROLIFERATING CELL NUCLEAR ANTIGEN

Expression of gene CG59613-01 was assessed using the primer-probe set Ag3496, described in Table CWA. Results of the RTQ-PCR runs are shown in Tables CWB and CWC.

Table CWA. Probe Name Ag3496

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-cacataccactgtgaccacaac-3'	22	238	707
Probe	TET-5'-cctcaccagcatgtccaaaatgctaa-3'- TAMRA	26	277	708
Reverse	5'-tgtcttccactgccattgttgta-3'	22	305	709

Table CWB. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3496, Run 217217871	Tissue Name	Rel. Exp.(%) Ag3496, Run 217217871
Adipose	9.6	Renal ca. TK-10	21.8
Melanoma* Hs688(A).T	25.2	Bladder	11.4
Melanoma* Hs688(B).T	20.4	Gastric ca. (liver met.) NCI-N87	3.9
Melanoma* M14	0.0	Gastric ca. KATO III	1.1
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.0
Melanoma* SK- MEL-5	1.5	Colon ca. SW480	1.7
Squamous cell carcinoma SCC-4	5.4	Colon ca.* (SW480 met) SW620	2.0
Testis Pool	56.3	Colon ca. HT29	3.9
Prostate ca.* (bone met) PC-3	2.6	Colon ca. HCT-116	12.9
Prostate Pool	37.6	Colon ca. CaCo-2	8.4
Placenta	0.0	Colon cancer tissue	1.4
Uterus Pool	21.5	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	18.3	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV- 3	1.9	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	8.0	Colon Pool	29.9
Ovarian ca. OVCAR-5	2.9	Small Intestine Pool	57.8

Ovarian ca. IGROV-1	0.0	Stomach Pool	38.7
Ovarian ca. OVCAR-8	0.0	Bone Marrow Pool	6.3
Ovary	4.9	Fetal Heart	6.2
Breast ca. MCF-7	4.3	Heart Pool	12.3
Breast ca. MDA-MB-231	6.4	Lymph Node Pool	64.6
Breast ca. BT 549	4.7	Fetal Skeletal Muscle	31.6
Breast ca. T47D	12.9	Skeletal Muscle Pool	0.0
Breast ca. MDA-N	0.0	Spleen Pool	1.7
Breast Pool	47.6	Thymus Pool	47.3
Trachea	26.1	CNS cancer (glio/astro) U87-MG	2.3
Lung	7.7	CNS cancer (glio/astro) U-118-MG	22.5
Fetal Lung	82.9	CNS cancer (neuro;met) SK-N-AS	0.9
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF-539	1.8
Lung ca. LX-1	0.0	CNS cancer (astro) SNB-75	35.4
Lung ca. NCI-H146	0.0	CNS cancer (glio) SNB-19	0.0
Lung ca. SHP-77	3.7	CNS cancer (glio) SF-295	9.2
Lung ca. A549	0.0	Brain (Amygdala) Pool	0.0
Lung ca. NCI-H526	0.0	Brain (cerebellum)	0.0
Lung ca. NCI-H23	46.0	Brain (fetal)	23.8
Lung ca. NCI-H460	0.5	Brain (Hippocampus) Pool	0.0
Lung ca. HOP-62	7.5	Cerebral Cortex Pool	1.6
Lung ca. NCI-H522	2.1	Brain (Substantia nigra) Pool	3.8
Liver	0.0	Brain (Thalamus) Pool	3.2
Fetal Liver	7.9	Brain (whole)	4.2
Liver ca. HepG2	0.0	Spinal Cord Pool	1.9
Kidney Pool	80.7	Adrenal Gland	1.7
Fetal Kidney	100.0	Pituitary gland Pool	0.7
Renal ca. 786-0	13.3	Salivary Gland	6.2
Renal ca. A498	0.0	Thyroid (female)	2.6
Renal ca. ACHN	23.8	Pancreatic ca. CAPAN2	5.5
Renal ca. UO-31	13.7	Pancreas Pool	48.6

Table CWC. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3496, Run 166441888	Tissue Name	Rel. Exp.(%) Ag3496, Run 166441888
Secondary Th1 act	0.0	HUVEC IL-1beta	0.7
Secondary Th2 act	0.7	HUVEC IFN gamma	1.0
Secondary Tr1 act	0.0	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	0.7	HUVEC TNF alpha + IL4	0.6
Secondary Th2 rest	1.2	HUVEC IL-11	0.4
Secondary Tr1 rest	0.4	Lung Microvascular EC none	1.0
Primary Th1 act	0.3	Lung Microvascular EC TNFalpha + IL-1beta	1.0
Primary Th2 act	1.2	Microvascular Dermal EC none	0.4
Primary Tr1 act	0.8	Microvascular Dermal EC TNFalpha + IL-1beta	0.2
Primary Th1 rest	1.5	Bronchial epithelium TNFalpha + IL1beta	5.2
Primary Th2 rest	1.0	Small airway epithelium none	6.6
Primary Tr1 rest	1.5	Small airway epithelium TNFalpha + IL-1beta	100.0
CD45RA CD4 lymphocyte act	2.1	Coronary artery SMC rest	2.6
CD45RO CD4 lymphocyte act	0.9	Coronary artery SMC TNFalpha + IL-1beta	1.5
CD8 lymphocyte act	2.1	Astrocytes rest	13.1
Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFalpha + IL-1beta	7.4
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	4.2
CD4 lymphocyte none	1.8	KU-812 (Basophil) PMA/ionomycin	5.2
2ry Th1/Th2/Tr1_anti- CD95 CH11	0.7	CCD1106 (Keratinocytes) none	17.9
LAK cells rest	0.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	82.4
LAK cells IL-2	2.3	Liver cirrhosis	17.2
LAK cells IL-2+IL-12	1.7	Lupus kidney	9.3
LAK cells IL-2+IFN gamma	2.3	NCI-H292 none	0.3
LAK cells IL-2+ IL-18	3.1	NCI-H292 IL-4	0.8

LAK cells PMA/ionomycin	0.2	NCI-H292 IL-9	3.0
NK Cells IL-2 rest	2.7	NCI-H292 IL-13	1.9
Two Way MLR 3 day	3.3	NCI-H292 IFN gamma	0.5
Two Way MLR 5 day	0.0	HPAEC none	0.3
Two Way MLR 7 day	0.2	HPAEC TNF alpha + IL-1 beta	0.6
PBMC rest	1.0	Lung fibroblast none	12.3
PBMC PWM	1.7	Lung fibroblast TNF alpha + IL-1 beta	2.9
PBMC PHA-L	0.7	Lung fibroblast IL-4	11.0
Ramos (B cell) none	0.0	Lung fibroblast IL-9	5.3
Ramos (B cell) ionomycin	0.0	Lung fibroblast IL-13	10.4
B lymphocytes PWM	0.9	Lung fibroblast IFN gamma	11.9
B lymphocytes CD40L and IL-4	2.8	Dermal fibroblast CCD1070 rest	11.7
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 TNF alpha	5.8
EOL-1 dbcAMP PMA/ionomycin	0.9	Dermal fibroblast CCD1070 IL-1 beta	2.3
Dendritic cells none	0.1	Dermal fibroblast IFN gamma	8.8
Dendritic cells LPS	0.7	Dermal fibroblast IL-4	11.3
Dendritic cells anti- CD40	0.6	IBD Colitis 2	2.6
Monocytes rest	0.7	IBD Crohn's	1.3
Monocytes LPS	0.0	Colon	11.4
Macrophages rest	0.0	Lung	1.9
Macrophages LPS	0.0	Thymus	3.8
HUVEC none	1.0	Kidney	7.2
HUVEC starved	1.4		

CNS_neurodegeneration_v1.0 Summary: Ag3496 Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.4 Summary: Ag3496 Expression of the CG59613-01 gene is highest in fetal and adult kidney (CTs = 31). This gene is also expressed at higher levels in fetal lung (CT = 31.4) than in adult lung (CT = 34.8), suggesting that expression of this gene can be used to distinguish adult and fetal lung and that this gene may play a role in lung

development and regeneration. Differentially higher expression in fetal tissues also occurs in brain and skeletal muscle.

In general, expression of this gene is associated with normal tissues rather than cancer cell lines. Specifically, CG59613-01 gene expression is downregulated in pancreatic, colon, gastric, renal, lung, breast and prostate cancer cell lines when compared to their respective normal tissues. Therefore, therapeutic modulation of the activity of this gene may be of benefit in the treatment of these cancers.

Among tissues with metabolic or endocrine function, this gene is expressed at low levels in pancreas, adipose, adrenal gland, fetal skeletal muscle, and the gastrointestinal tract. Therefore, therapeutic modulation of the activity of this gene may prove useful in the treatment of endocrine/metabolically related diseases, such as obesity and diabetes.

Panel 4D Summary: Ag3496 Expression of the CG59613-01 gene is highest in small airway epithelium treated with TNF alpha and IL-1 beta (CT = 29.4). In addition, this gene is substantially upregulated in keratinocytes treated with TNF alpha and IL-1 beta. Low expression of this gene is also seen in lung and dermal fibroblasts independent of treatment. Therefore, therapeutics designed with the protein encoded by the transcript may reduce or eliminate symptoms caused by inflammation of the lung and skin in chronic obstructive pulmonary disease, asthma, allergy, emphysema, and psoriasis.

CX. CG59619-01: ACTIN, CYTOPLASMIC 2

Expression of gene CG59619-01 was assessed using the primer-probe set Ag3498, described in Table CXA. Results of the RTQ-PCR runs are shown in Tables CXB and CXC.

Table CXA. Probe Name Ag3498

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-tgatatggacatccccaag-3'	20	860	710
Probe	TET-5'-acctgtacgccaacacagtgtgtct-3'- TAMRA	26	880	711
Reverse	5'-atctccttctgcatacctattgg-3'	22	934	712

Table CXB. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3498,	Tissue Name	Rel. Exp.(%) Ag3498,
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	Run 217217873		Run 217217873
Adipose	4.7	Renal ca. TK-10	0.0
Melanoma* Hs688(A).T	0.0	Bladder	3.3
Melanoma* Hs688(B).T	0.0	Gastric ca. (liver met.) NCI-N87	0.0
Melanoma* M14	0.0	Gastric ca. KATO III	0.0
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.0
Melanoma* SK- MEL-5	0.0	Colon ca. SW480	0.0
Squamous cell carcinoma SCC-4	0.0	Colon ca.* (SW480 met) SW620	0.0
Testis Pool	55.1	Colon ca. HT29	0.0
Prostate ca.* (bone met) PC-3	0.0	Colon ca. HCT-116	8.7
Prostate Pool	0.0	Colon ca. CaCo-2	4.9
Placenta	0.0	Colon cancer tissue	0.0
Uterus Pool	0.0	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	6.6	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV- 3	9.5	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	0.0	Colon Pool	18.3
Ovarian ca. OVCAR-5	17.9	Small Intestine Pool	26.2
Ovarian ca. IGROV- 1	0.0	Stomach Pool	7.2
Ovarian ca. OVCAR-8	0.0	Bone Marrow Pool	0.0
Ovary	2.9	Fetal Heart	6.4
Breast ca. MCF-7	0.0	Heart Pool	11.2
Breast ca. MDA- MB-231	0.0	Lymph Node Pool	34.2
Breast ca. BT 549	8.4	Fetal Skeletal Muscle	12.9
Breast ca. T47D	2.5	Skeletal Muscle Pool	10.8
Breast ca. MDA-N	0.0	Spleen Pool	4.7
Breast Pool	13.7	Thymus Pool	27.0
Trachea	5.4	CNS cancer (glio/astro) U87-MG	0.0
Lung	7.0	CNS cancer (glio/astro) U-118-MG	2.2
Fetal Lung	7.9	CNS cancer	0.0

		(neuro;met) SK-N-AS	
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF-539	0.0
Lung ca. LX-1	0.0	CNS cancer (astro) SNB-75	0.0
Lung ca. NCI-H146	3.1	CNS cancer (glio) SNB-19	0.0
Lung ca. SHP-77	0.0	CNS cancer (glio) SF-295	0.0
Lung ca. A549	0.0	Brain (Amygdala) Pool	12.9
Lung ca. NCI-H526	0.0	Brain (cerebellum)	3.2
Lung ca. NCI-H23	0.0	Brain (fetal)	12.9
Lung ca. NCI-H460	0.0	Brain (Hippocampus) Pool	6.0
Lung ca. HOP-62	0.0	Cerebral Cortex Pool	4.9
Lung ca. NCI-H522	0.0	Brain (Substantia nigra) Pool	26.6
Liver	0.0	Brain (Thalamus) Pool	37.9
Fetal Liver	0.0	Brain (whole)	0.0
Liver ca. HepG2	0.0	Spinal Cord Pool	0.0
Kidney Pool	100.0	Adrenal Gland	0.0
Fetal Kidney	4.4	Pituitary gland Pool	0.0
Renal ca. 786-0	0.0	Salivary Gland	0.0
Renal ca. A498	0.0	Thyroid (female)	0.0
Renal ca. ACHN	0.0	Pancreatic ca. CAPAN2	6.5
Renal ca. UO-31	0.0	Pancreas Pool	6.3

Table CXC. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag3498, Run 169839576	Tissue Name	Rel. Exp.(%) Ag3498, Run 169839576
Secondary Th1 act	78.5	HUVEC IL-1beta	11.3
Secondary Th2 act	17.0	HUVEC IFN gamma	12.4
Secondary Tr1 act	17.9	HUVEC TNF alpha + IFN gamma	15.7
Secondary Th1 rest	5.2	HUVEC TNF alpha + IL4	12.5
Secondary Th2 rest	7.0	HUVEC IL-11	5.4
Secondary Tr1 rest	5.5	Lung Microvascular EC none	17.2
Primary Th1 act	14.8	Lung Microvascular EC TNFalpha + IL-1beta	7.6
Primary Th2 act	16.0	Microvascular Dermal EC none	8.1

Primary Tr1 act	13.3	Microsvascular Dermal EC TNFalpha + IL-1beta	8.0
Primary Th1 rest	8.2	Bronchial epithelium TNFalpha + IL1beta	5.3
Primary Th2 rest	7.1	Small airway epithelium none	4.3
Primary Tr1 rest	8.1	Small airway epithelium TNFalpha + IL-1beta	6.4
CD45RA CD4 lymphocyte act	15.8	Coronary artery SMC rest	5.8
CD45RO CD4 lymphocyte act	15.9	Coronary artery SMC TNFalpha + IL-1beta	5.9
CD8 lymphocyte act	19.6	Astrocytes rest	6.2
Secondary CD8 lymphocyte rest	14.0	Astrocytes TNFalpha + IL-1beta	4.6
Secondary CD8 lymphocyte act	9.7	KU-812 (Basophil) rest	34.4
CD4 lymphocyte none	4.3	KU-812 (Basophil) PMA/ionomycin	31.9
2ry Th1/Th2/Tr1 _anti- CD95 CH11	6.1	CCD1106 (Keratinocytes) none	28.9
LAK cells rest	12.6	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	34.2
LAK cells IL-2	9.9	Liver cirrhosis	1.4
LAK cells IL-2+IL-12	12.6	NCI-H292 none	9.3
LAK cells IL-2+IFN gamma	9.4	NCI-H292 IL-4	13.1
LAK cells IL-2+ IL-18	12.5	NCI-H292 IL-9	17.7
LAK cells PMA/ionomycin	13.9	NCI-H292 IL-13	13.6
NK Cells IL-2 rest	15.5	NCI-H292 IFN gamma	22.2
Two Way MLR 3 day	13.0	HPAEC none	4.4
Two Way MLR 5 day	14.4	HPAEC TNF alpha + IL-1 beta	12.4
Two Way MLR 7 day	8.8	Lung fibroblast none	5.7
PBMC rest	6.6	Lung fibroblast TNF alpha + IL-1 beta	14.6
PBMC PWM	16.8	Lung fibroblast IL-4	8.8
PBMC PHA-L	15.1	Lung fibroblast IL-9	13.0
Ramos (B cell) none	13.0	Lung fibroblast IL-13	10.2
Ramos (B cell) ionomycin	11.4	Lung fibroblast IFN gamma	17.8
B lymphocytes PWM	13.7	Dermal fibroblast CCD1070 rest	9.8
B lymphocytes CD40L	13.8	Dermal fibroblast	10.8

and IL-4		CCD1070 TNF alpha	
EOL-1 dbcAMP	11.1	Dermal fibroblast CCD1070 IL-1 beta	11.2
EOL-1 dbcAMP PMA/ionomycin	100.0	Dermal fibroblast IFN gamma	19.8
Dendritic cells none	14.4	Dermal fibroblast IL-4	9.7
Dendritic cells LPS	9.8	Dermal Fibroblasts rest	7.7
Dendritic cells anti- CD40	13.2	Neutrophils TNFa+LPS	0.7
Monocytes rest	8.9	Neutrophils rest	1.1
Monocytes LPS	32.5	Colon	4.4
Macrophages rest	12.6	Lung	5.1
Macrophages LPS	17.3	Thymus	7.3
HUVEC none	6.2	Kidney	4.9
HUVEC starved	10.0		

CNS_neurodegeneration_v1.0 Summary: Ag3498 Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.4 Summary: Ag3498 The CG59619-01 gene is only expressed at detectable levels in the adult kidney (CT = 34.2). Thus, expression of this gene can be used to distinguish kidney from the other samples on this panel. In addition, expression of this gene is much lower in fetal kidney (CT = 38.7), suggesting that this gene can be used to distinguish between the fetal and adult source of this tissue. Furthermore, this gene is not expressed at detectable levels in renal cancer cell lines. Therefore, therapeutic modulation of this gene may be of use in the treatment of renal cell carcinoma.

Panel 4.1D Summary: Ag3498 Expression of the CG59619-01 gene is highest in activated eosinophils (CT = 25.7), displaying 10-fold upregulation when compared to the control eosinophils. Therefore, therapies designed with the protein encoded for by this gene could block or inhibit inflammation or tissue damage due to eosinophil activation in response to asthma, ulcerative colitis and parasitic diseases.

The CG59619-01 gene is expressed at moderate levels in the majority of samples on this panel, including T cells, B cells, endothelial cells, macrophages, monocytes, dendritic cells, basophils and peripheral blood mononuclear cells, as well as epithelial and fibroblast cell types from lung and skin, and normal tissues represented by colon, lung, thymus and kidney. This ubiquitous pattern of expression suggests that this gene product may be involved in

homeostatic processes for these and other cell types and tissues. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

CY. CG59621-01: SELENIDE, WATER DIKINASE 1

Expression of gene CG59621-01 was assessed using the primer-probe set Ag3764, described in Table CYA.

Table CYA. Probe Name Ag3764

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-catgttcagcctcatgcat-3'	19	925	713
Probe	TET-5'-agacctcaggcggccttctgatct-3'- TAMRA	24	957	714
Reverse	5'-ctgcttgctgacatggtaaac-3'	21	981	715

General_screening_panel_v1.4 Summary: Ag3764 Results from one experiment with the CG59621-01 gene are not included. The amp plot indicates that there were experimental difficulties with this run.

Panel 4.1D Summary: Ag3764 Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

CZ. CG59625-01: GLUCOSE TRANSPORTER TYPE 3

Expression of gene CG59625-01 was assessed using the primer-probe set Ag3499, described in Table CZA. Results of the RTQ-PCR runs are shown in Tables CZB and CZC.

Table CZA. Probe Name Ag3499

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-cttccccctctgctgcttactat-3'	22	1298	716
Probe	TET-5'-ttttattatcttcaccggcttcctca-3'- TAMRA	26	1334	717
Reverse	5'-gaaggtaaaggccaagaaggta-3'	22	1361	718

Table CZB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3499, Run 210935864	Tissue Name	Rel. Exp.(%) Ag3499, Run 210935864
AD 1 Hippo	5.8	Control (Path) 3 Temporal Ctx	4.9
AD 2 Hippo	25.9	Control (Path) 4 Temporal Ctx	32.3
AD 3 Hippo	5.8	AD 1 Occipital Ctx	11.6
AD 4 Hippo	1.5	AD 2 Occipital Ctx (Missing)	0.0
AD 5 hippo	100.0	AD 3 Occipital Ctx	5.1
AD 6 Hippo	29.7	AD 4 Occipital Ctx	4.5
Control 2 Hippo	31.9	AD 5 Occipital Ctx	39.2
Control 4 Hippo	0.0	AD 6 Occipital Ctx	72.2
Control (Path) 3 Hippo	6.6	Control 1 Occipital Ctx	13.5
AD 1 Temporal Ctx	7.0	Control 2 Occipital Ctx	82.4
AD 2 Temporal Ctx	49.3	Control 3 Occipital Ctx	8.8
AD 3 Temporal Ctx	2.9	Control 4 Occipital Ctx	0.0
AD 4 Temporal Ctx	5.6	Control (Path) 1 Occipital Ctx	64.6
AD 5 Inf Temporal Ctx	83.5	Control (Path) 2 Occipital Ctx	4.0
AD 5 SupTemporal Ctx	37.6	Control (Path) 3 Occipital Ctx	4.0
AD 6 Inf Temporal Ctx	23.0	Control (Path) 4 Occipital Ctx	13.2
AD 6 Sup Temporal Ctx	24.8	Control 1 Parietal Ctx	9.9
Control 1 Temporal Ctx	11.0	Control 2 Parietal Ctx	33.2
Control 2 Temporal Ctx	50.7	Control 3 Parietal Ctx	12.1
Control 3 Temporal Ctx	6.0	Control (Path) 1 Parietal Ctx	57.8
Control 4 Temporal Ctx	0.1	Control (Path) 2 Parietal Ctx	25.2
Control (Path) 1 Temporal Ctx	28.9	Control (Path) 3 Parietal Ctx	5.6
Control (Path) 2 Temporal Ctx	13.9	Control (Path) 4 Parietal Ctx	60.3

Table CZC. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3499, Run 166441940	Tissue Name	Rel. Exp.(%) Ag3499, Run 166441940
Secondary Th1 act	12.1	HUVEC IL-1beta	0.1
Secondary Th2 act	3.2	HUVEC IFN gamma	3.2
Secondary Tr1 act	3.6	HUVEC TNF alpha + IFN gamma	0.1
Secondary Th1 rest	7.5	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	5.3	HUVEC IL-11	0.9
Secondary Tr1 rest	6.0	Lung Microvascular EC none	2.0
Primary Th1 act	2.4	Lung Microvascular EC TNFalpha + IL-1beta	1.2
Primary Th2 act	7.5	Microvascular Dermal EC none	0.1
Primary Tr1 act	10.1	Microvascular Dermal EC TNFalpha + IL-1beta	0.1
Primary Th1 rest	14.9	Bronchial epithelium TNFalpha + IL1beta	0.3
Primary Th2 rest	5.1	Small airway epithelium none	0.3
Primary Tr1 rest	5.8	Small airway epithelium TNFalpha + IL-1beta	1.9
CD45RA CD4 lymphocyte act	2.9	Coronary artery SMC rest	2.4
CD45RO CD4 lymphocyte act	12.3	Coronary artery SMC TNFalpha + IL-1beta	1.3
CD8 lymphocyte act	4.1	Astrocytes rest	0.3
Secondary CD8 lymphocyte rest	4.3	Astrocytes TNFalpha + IL-1beta	0.5
Secondary CD8 lymphocyte act	2.9	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	3.2	KU-812 (Basophil) PMA/ionomycin	0.3
2ry Th1/Th2/Tr1_anti- CD95 CH11	6.4	CCD1106 (Keratinocytes) none	1.9
LAK cells rest	8.9	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	30.6
LAK cells IL-2	14.1	Liver cirrhosis	19.2
LAK cells IL-2+IL-12	7.1	Lupus kidney	1.5
LAK cells IL-2+IFN gamma	8.2	NCI-H292 none	0.5
LAK cells IL-2+ IL-18	6.3	NCI-H292 IL-4	0.8

LAK cells PMA/ionomycin	100.0	NCI-H292 IL-9	0.2
NK Cells IL-2 rest	4.8	NCI-H292 IL-13	0.3
Two Way MLR 3 day	7.4	NCI-H292 IFN gamma	0.2
Two Way MLR 5 day	7.6	HPAEC none	1.7
Two Way MLR 7 day	3.8	HPAEC TNF alpha + IL-1 beta	1.5
PBMC rest	0.1	Lung fibroblast none	3.2
PBMC PWM	10.9	Lung fibroblast TNF alpha + IL-1 beta	2.7
PBMC PHA-L	9.2	Lung fibroblast IL-4	4.7
Ramos (B cell) none	0.3	Lung fibroblast IL-9	2.4
Ramos (B cell) ionomycin	0.2	Lung fibroblast IL-13	3.0
B lymphocytes PWM	3.8	Lung fibroblast IFN gamma	5.5
B lymphocytes CD40L and IL-4	2.6	Dermal fibroblast CCD1070 rest	3.7
EOL-1 dbcAMP	0.1	Dermal fibroblast CCD1070 TNF alpha	15.1
EOL-1 dbcAMP PMA/ionomycin	0.6	Dermal fibroblast CCD1070 IL-1 beta	2.5
Dendritic cells none	30.4	Dermal fibroblast IFN gamma	0.1
Dendritic cells LPS	14.2	Dermal fibroblast IL-4	0.1
Dendritic cells anti- CD40	15.1	IBD Colitis 2	0.0
Monocytes rest	5.8	IBD Crohn's	1.1
Monocytes LPS	12.1	Colon	3.3
Macrophages rest	0.3	Lung	7.9
Macrophages LPS	12.9	Thymus	0.6
HUVEC none	0.1	Kidney	9.4
HUVEC starved	0.1		

CNS_neurodegeneration_v1.0 Summary: Ag3499 This panel confirms the expression of this gene at moderate levels in the brains of an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. Please see Panel 1.4 for a discussion of the potential utility of this gene in treatment of central nervous system disorders.

Panel 4D Summary: Ag3499 Expression of the CG59625-01 gene is highest in PMA/ionomycin-treated lymphokine activated killer (LAK) cells (CT = 24.3). Since these

cells are involved in tumor immunology and tumor cell clearance, as well as virally and bacterial infected cells, therapeutic modulation of this gene product may alter the functions of these cells and lead to improvement in cancer cell killing as well as host immunity to microbial and viral infections.

This gene is also expressed at high levels in stimulated keratinocytes, dendritic cells, monocytes and macrophages, suggesting that small molecule therapeutics designed against the CG59625-01 protein could reduce or inhibit inflammation in asthma, emphysema, allergy, psoriasis, arthritis, or any other condition in which localization/activation of these cell types is important.

This gene is also expressed at moderate levels in a number of other cell types of significance in the immune response in health and disease.

DA. CG59887-01 and CG59887-02: Amino Acid/Metabolite Permease

Expression of gene CG59887-01 and full length clone CG59887-02 was assessed using the primer-probe set Ag4715, described in Table DAA. Please note that CG59887-02 represents a full-length physical clone of the CG59887-02 gene, validating the prediction of the gene sequence.

Table DAA. Probe Name Ag4715

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-cgtggttggtggttgtttt-3'	20	1362	719
Probe	TET-5'-actgcgcacgcgccttaacaatg-3'-TAMRA	23	1383	720
Reverse	5'-ggctagtggtcgagcaattt-3'	20	1426	721

General_screening_panel_v1.4 Summary: Ag4715 Expression of the CG59887-01 gene is low/undetectable in all samples on this panel (CTs>35). (Data not shown.) The amp plot indicates that there is a high probability of a probe failure.

DB. CG59857-01: RHOTEKIN

Expression of gene CG59857-01 was assessed using the primer-probe set Ag3622, described in Table DBA. Results of the RTQ-PCR runs are shown in Tables DBB, DBC and DBD.

Table DBA. Probe Name Ag3622

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-acatcctggaggacctgaatat-3'	22	84	722
Probe	TET-5'-ctctacattcggcagatggcactcag-3'- TAMRA	26	107	723
Reverse	5'-ggatctcatggtctagcttct-3'	22	155	724

Table DBB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3622, Run 211005293	Tissue Name	Rel. Exp.(%) Ag3622, Run 211005293
AD 1 Hippo	10.7	Control (Path) 3 Temporal Ctx	3.9
AD 2 Hippo	42.9	Control (Path) 4 Temporal Ctx	9.2
AD 3 Hippo	6.9	AD 1 Occipital Ctx	10.1
AD 4 Hippo	13.2	AD 2 Occipital Ctx (Missing)	0.0
AD 5 Hippo	40.6	AD 3 Occipital Ctx	7.1
AD 6 Hippo	38.4	AD 4 Occipital Ctx	23.3
Control 2 Hippo	29.9	AD 5 Occipital Ctx	28.5
Control 4 Hippo	13.6	AD 6 Occipital Ctx	0.1
Control (Path) 3 Hippo	0.8	Control 1 Occipital Ctx	4.9
AD 1 Temporal Ctx	17.8	Control 2 Occipital Ctx	51.4
AD 2 Temporal Ctx	27.7	Control 3 Occipital Ctx	12.2
AD 3 Temporal Ctx	6.3	Control 4 Occipital Ctx	8.2
AD 4 Temporal Ctx	19.5	Control (Path) 1 Occipital Ctx	58.6
AD 5 Inf Temporal Ctx	100.0	Control (Path) 2 Occipital Ctx	10.2
AD 5 Sup Temporal Ctx	47.3	Control (Path) 3 Occipital Ctx	5.7
AD 6 Inf Temporal Ctx	49.0	Control (Path) 4 Occipital Ctx	7.9

AD 6 Sup Temporal Ctx	29.7	Control 1 Parietal Ctx	7.6
Control 1 Temporal Ctx	5.6	Control 2 Parietal Ctx	44.4
Control 2 Temporal Ctx	34.9	Control 3 Parietal Ctx	16.2
Control 3 Temporal Ctx	13.7	Control (Path) 1 Parietal Ctx	32.1
Control 3 Temporal Ctx	8.2	Control (Path) 2 Parietal Ctx	15.6
Control (Path) 1 Temporal Ctx	18.8	Control (Path) 3 Parietal Ctx	2.4
Control (Path) 2 Temporal Ctx	16.0	Control (Path) 4 Parietal Ctx	17.6

Table DBC. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3622, Run 218211380	Rel. Exp.(%) Ag3622, Run 218307304	Tissue Name	Rel. Exp.(%) Ag3622, Run 218211380	Rel. Exp.(%) Ag3622, Run 218307304
Adipose	0.7	1.1	Renal ca. TK-10	4.7	4.0
Melanoma* Hs688(A).T	4.6	7.6	Bladder	10.2	3.5
Melanoma* Hs688(B).T	7.2	6.4	Gastric ca. (liver met.) NCI-N87	6.0	9.0
Melanoma* M14	29.9	37.9	Gastric ca. KATO III	7.8	7.7
Melanoma* LOXIMVI	15.1	17.2	Colon ca. SW- 948	1.9	1.3
Melanoma* SK-MEL-5	19.3	22.7	Colon ca. SW480	11.0	15.1
Squamous cell carcinoma SCC-4	0.4	1.5	Colon ca.* (SW480 met) SW620	5.9	10.4
Testis Pool	2.0	1.7	Colon ca. HT29	5.4	6.8
Prostate ca.* (bone met) PC-3	3.3	3.4	Colon ca. HCT- 116	5.6	6.7
Prostate Pool	0.8	2.3	Colon ca. CaCo-2	4.2	3.2
Placenta	2.2	3.0	Colon cancer tissue	2.3	3.5
Uterus Pool	0.8	0.7	Colon ca. SW1116	1.1	2.9
Ovarian ca. OVCAR-3	19.5	18.7	Colon ca. Colo- 205	1.0	0.3

Ovarian ca. SK-OV-3	9.0	8.0	Colon ca. SW-48	1.2	1.2
Ovarian ca. OVCAR-4	1.1	2.2	Colon Pool	16.0	5.8
Ovarian ca. OVCAR-5	6.4	9.0	Small Intestine Pool	1.7	3.3
Ovarian ca. IGROV-1	10.7	10.7	Stomach Pool	2.7	3.8
Ovarian ca. OVCAR-8	7.1	20.3	Bone Marrow Pool	1.2	1.8
Ovary	3.2	4.3	Fetal Heart	5.1	6.5
Breast ca. MCF-7	1.1	1.4	Heart Pool	1.5	3.0
Breast ca. MDA-MB- 231	8.8	10.9	Lymph Node Pool	4.9	6.5
Breast ca. BT 549	4.7	8.4	Fetal Skeletal Muscle	69.7	11.3
Breast ca. T47D	17.0	15.2	Skeletal Muscle Pool	2.7	1.5
Breast ca. MDA-N	23.8	21.0	Spleen Pool	2.8	1.8
Breast Pool	4.4	5.0	Thymus Pool	2.8	5.9
Trachea	3.8	5.8	CNS cancer (glio/astro) U87- MG	17.7	25.0
Lung	0.7	0.8	CNS cancer (glio/astro) U- 118-MG	46.0	57.4
Fetal Lung	8.2	9.3	CNS cancer (neuro;met) SK- N-AS	26.8	35.6
Lung ca. NCI- N417	0.4	0.5	CNS cancer (astro) SF-539	9.7	9.8
Lung ca. LX- 1	9.3	10.7	CNS cancer (astro) SNB-75	22.5	34.4
Lung ca. NCI- H146	8.4	6.7	CNS cancer (glio) SNB-19	9.0	13.0
Lung ca. SHP-77	7.4	6.4	CNS cancer (glio) SF-295	33.2	37.1
Lung ca. A549	13.3	23.3	Brain (Amygdala) Pool	86.5	82.9
Lung ca. NCI- H526	1.3	1.4	Brain (cerebellum)	22.5	30.8
Lung ca. NCI- H23	5.1	6.0	Brain (fetal)	5.1	6.5

Lung ca. NCI-H460	5.2	4.9	Brain (Hippocampus) Pool	45.4	52.1
Lung ca. HOP-62	5.1	7.4	Cerebral Cortex Pool	27.4	40.3
Lung ca. NCI-H522	6.7	9.8	Brain (Substantia nigra) Pool	46.7	54.7
Liver	0.5	0.9	Brain (Thalamus) Pool	51.4	90.1
Fetal Liver	1.7	1.5	Brain (whole)	23.8	32.8
Liver ca. HepG2	2.9	4.5	Spinal Cord Pool	100.0	100.0
Kidney Pool	5.3	6.4	Adrenal Gland	1.5	3.5
Fetal Kidney	7.0	11.7	Pituitary gland Pool	0.3	2.5
Renal ca. 786-0	2.8	3.0	Salivary Gland	1.4	3.2
Renal ca. A498	4.9	5.6	Thyroid (female)	2.8	2.1
Renal ca. ACHN	4.2	4.0	Pancreatic ca. CAPAN2	1.7	0.6
Renal ca. UO-31	10.4	7.7	Pancreas Pool	5.2	6.2

Table DBD. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag3622, Run 169944131	Tissue Name	Rel. Exp.(%) Ag3622, Run 169944131
Secondary Th1 act	0.0	HUVEC IL-1beta	14.7
Secondary Th2 act	2.9	HUVEC IFN gamma	25.2
Secondary Tr1 act	7.3	HUVEC TNF alpha + IFN gamma	2.5
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	5.8
Secondary Th2 rest	0.0	HUVEC IL-11	19.2
Secondary Tr1 rest	0.0	Lung Microvascular EC none	49.0
Primary Th1 act	6.5	Lung Microvascular EC TNFalpha + IL-1beta	11.3
Primary Th2 act	0.0	Microvascular Dermal EC none	7.7
Primary Tr1 act	0.0	Microvascular Dermal EC TNFalpha + IL-1beta	10.9
Primary Th1 rest	0.0	Bronchial epithelium TNFalpha + IL1beta	21.5

Primary Th2 rest	0.0	Small airway epithelium none	7.2
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	27.9
CD45RA CD4 lymphocyte act	0.8	Coronary artery SMC rest	22.5
CD45RO CD4 lymphocyte act	3.5	Coronary artery SMC TNFalpha + IL-1beta	31.4
CD8 lymphocyte act	1.8	Astrocytes rest	17.0
Secondary CD8 lymphocyte rest	1.6	Astrocytes TNFalpha + IL-1beta	25.3
Secondary CD8 lymphocyte act	0.2	KU-812 (Basophil) rest	8.0
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	3.4
2ry Th1/Th2/Tr1_anti-CD95 CH11	4.2	CCD1106 (Keratinocytes) none	44.8
LAK cells rest	0.4	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	61.6
LAK cells IL-2	6.0	Liver cirrhosis	0.0
LAK cells IL-2+IL-12	0.0	NCI-H292 none	5.3
LAK cells IL-2+IFN gamma	1.5	NCI-H292 IL-4	9.9
LAK cells IL-2+ IL-18	0.0	NCI-H292 IL-9	14.4
LAK cells PMA/ionomycin	0.0	NCI-H292 IL-13	1.4
NK Cells IL-2 rest	13.9	NCI-H292 IFN gamma	11.4
Two Way MLR 3 day	3.6	HPAEC none	20.9
Two Way MLR 5 day	3.8	HPAEC TNF alpha + IL-1 beta	10.2
Two Way MLR 7 day	0.0	Lung fibroblast none	38.2
PBMC rest	1.7	Lung fibroblast TNF alpha + IL-1 beta	25.0
PBMC PWM	3.6	Lung fibroblast IL-4	35.8
PBMC PHA-L	1.3	Lung fibroblast IL-9	100.0
Ramos (B cell) none	0.2	Lung fibroblast IL-13	69.7
Ramos (B cell) ionomycin	1.1	Lung fibroblast IFN gamma	58.2
B lymphocytes PWM	0.5	Dermal fibroblast CCD1070 rest	39.2
B lymphocytes CD40L and IL-4	7.9	Dermal fibroblast CCD1070 TNF alpha	5.7
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 IL-1 beta	17.4
EOL-1 dbcAMP	0.0	Dermal fibroblast IFN	31.2

PMA/ionomycin		gamma	
Dendritic cells none	9.9	Dermal fibroblast IL-4	44.8
Dendritic cells LPS	2.4	Dermal Fibroblasts rest	19.1
Dendritic cells anti-CD40	24.7	Neutrophils TNFa+LPS	0.0
Monocytes rest	0.0	Neutrophils rest	0.0
Monocytes LPS	6.3	Colon	10.3
Macrophages rest	8.8	Lung	13.6
Macrophages LPS	3.4	Thymus	2.4
HUVEC none	11.1	Kidney	23.8
HUVEC starved	28.5		

CNS_neurodegeneration_v1.0 Summary: Ag3622 This panel confirms the expression of the CG59857-01 gene at significant levels in the brains of an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. Please see Panel 1.4 for a discussion of the potential utility of this gene in treatment of central nervous system disorders.

General_screening_panel_v1.4 Summary: Ag3622 Two experiments with the same probe and primer set show highest expression of the CG59857-01 gene in spinal cord samples (CTs=26-28). In addition, high levels of expression of this gene are seen in brain derived tissue, including samples from amygdala, hippocampus, substantia nigra, thalamus, cerebellum, cerebral cortex, and CNS cancer cell lines. Therefore, expression of this gene could be used to distinguish between brain derived samples and other samples used in this panel. Furthermore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

Significant expression is also detected in fetal skeletal muscle (CTs=27-31). Interestingly, this gene is expressed at much higher levels in fetal when compared to adult skeletal muscle (CTs=32-34). This observation suggests that expression of this gene can be used to distinguish fetal from adult skeletal muscle. In addition, the relative overexpression of this gene in fetal skeletal muscle suggests that the protein product may enhance muscular growth or development in the fetus and thus may also act in a regenerative capacity in the adult. Therefore, therapeutic modulation of the protein encoded by this gene could be useful in

treatment of muscle related diseases. More specifically, treatment of weak or dystrophic muscle with the protein encoded by this gene could restore muscle mass or function.

Among tissues with metabolic function, this gene is expressed at moderate to low levels in pituitary, adipose, adrenal gland, pancreas, thyroid, and adult and fetal skeletal muscle, heart, and liver. This widespread expression among these tissues suggests that this gene product may play a role in normal neuroendocrine and metabolic and that dysregulated expression of this gene may contribute to neuroendocrine disorders or metabolic diseases, such as obesity and diabetes.

Panel 4.1D Summary: Ag3622 Highest expression of the CG59857-01 gene is seen in IL-9/IL-13 treated lung fibroblasts (CT=31). In addition, significant expression is seen in clusters of treated and untreated lung and dermal fibroblasts, epithelium and endothelium. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, and psoriasis.

DC. CG59855-01 and CG59855-02: ATP SYNTHASE SUBUNIT C

Expression of gene CG59855-01 and full length clone CG59855-02 was assessed using the primer-probe set Ag3621, described in Table DCA. Results of the RTQ-PCR runs are shown in Tables DCB and DCC. Please note that CG59855-02 represents a full-length physical clone of the CG59855-02 gene, validating the prediction of the gene sequence.

Table DCA. Probe Name Ag3621

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-gggtctaatacaggectgtgt-3'	20	73	725
Probe	TET-5'-tgcccttcctcctgaatagcccagaga-3'-TAMRA	26	94	726
Reverse	5'-ctgctgttaggaaggctgtttag-3'	22	126	727

Table DCB. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3621, Run 217702346	Tissue Name	Rel. Exp.(%) Ag3621, Run 217702346
Adipose	0.0	Renal ca. TK-10	0.0

Melanoma* Hs688(A).T	0.0	Bladder	7.5
Melanoma* Hs688(B).T	0.0	Gastric ca. (liver met.) NCI-N87	0.0
Melanoma* M14	0.0	Gastric ca. KATO III	0.0
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.0
Melanoma* SK- MEL-5	0.0	Colon ca. SW480	0.0
Squamous cell carcinoma SCC-4	0.0	Colon ca.* (SW480 met) SW620	0.0
Testis Pool	35.1	Colon ca. HT29	0.0
Prostate ca.* (bone met) PC-3	0.0	Colon ca. HCT-116	0.0
Prostate Pool	3.5	Colon ca. CaCo-2	0.0
Placenta	2.9	Colon cancer tissue	0.0
Uterus Pool	5.9	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	0.0	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV- 3	47.6	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	0.0	Colon Pool	57.0
Ovarian ca. OVCAR-5	0.0	Small Intestine Pool	42.9
Ovarian ca. IGROV- 1	0.0	Stomach Pool	7.5
Ovarian ca. OVCAR-8	0.0	Bone Marrow Pool	7.0
Ovary	12.9	Fetal Heart	0.0
Breast ca. MCF-7	0.0	Heart Pool	0.0
Breast ca. MDA- MB-231	0.0	Lymph Node Pool	8.1
Breast ca. BT 549	0.0	Fetal Skeletal Muscle	13.2
Breast ca. T47D	0.0	Skeletal Muscle Pool	0.0
Breast ca. MDA-N	0.0	Spleen Pool	27.4
Breast Pool	49.0	Thymus Pool	25.9
Trachea	46.3	CNS cancer (glio/astro) U87-MG	0.0
Lung	38.4	CNS cancer (glio/astro) U-118-MG	0.0
Fetal Lung	100.0	CNS cancer (neuro;met) SK-N-AS	0.0
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF- 539	0.0

Lung ca. LX-1	0.0	CNS cancer (astro) SNB-75	0.0
Lung ca. NCI-H146	0.0	CNS cancer (glio) SNB-19	0.0
Lung ca. SHP-77	0.0	CNS cancer (glio) SF- 295	0.0
Lung ca. A549	0.0	Brain (Amygdala) Pool	0.0
Lung ca. NCI-H526	0.0	Brain (cerebellum)	0.0
Lung ca. NCI-H23	6.7	Brain (fetal)	0.0
Lung ca. NCI-H460	0.0	Brain (Hippocampus) Pool	0.0
Lung ca. HOP-62	0.0	Cerebral Cortex Pool	0.0
Lung ca. NCI-H522	0.0	Brain (Substantia nigra) Pool	0.0
Liver	0.0	Brain (Thalamus) Pool	0.0
Fetal Liver	0.0	Brain (whole)	0.0
Liver ca. HepG2	0.0	Spinal Cord Pool	6.1
Kidney Pool	57.8	Adrenal Gland	0.0
Fetal Kidney	10.7	Pituitary gland Pool	12.4
Renal ca. 786-0	0.0	Salivary Gland	0.0
Renal ca. A498	0.0	Thyroid (female)	0.0
Renal ca. ACHN	0.0	Pancreatic ca. CAPAN2	0.0
Renal ca. UO-31	0.0	Pancreas Pool	63.3

Table DCC. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag3621, Run 169944096	Tissue Name	Rel. Exp.(%) Ag3621, Run 169944096
Secondary Th1 act	1.0	HUVEC IL-1beta	0.0
Secondary Th2 act	0.0	HUVEC IFN gamma	1.0
Secondary Tr1 act	16.5	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	7.5	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	2.6	HUVEC IL-11	7.8
Secondary Tr1 rest	0.0	Lung Microvascular EC none	1.0
Primary Th1 act	0.0	Lung Microvascular EC TNFalpha + IL-1beta	6.7
Primary Th2 act	0.0	Microvascular Dermal EC none	0.0
Primary Tr1 act	0.0	Microvascular Dermal EC TNFalpha + IL-1beta	0.0
Primary Th1 rest	0.0	Bronchial epithelium	0.0

		TNFalpha + IL1beta	
Primary Th2 rest	1.5	Small airway epithelium none	0.0
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	0.0
CD45RA CD4 lymphocyte act	0.0	Coronary artery SMC rest	0.0
CD45RO CD4 lymphocyte act	0.0	Coronary artery SMC TNFalpha + IL-1beta	0.0
CD8 lymphocyte act	0.0	Astrocytes rest	1.1
Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFalpha + IL-1beta	0.9
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	8.6	KU-812 (Basophil) PMA/ionomycin	0.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.0	CCD1106 (Keratinocytes) none	0.0
LAK cells rest	0.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0
LAK cells IL-2	0.0	Liver cirrhosis	0.0
LAK cells IL-2+IL-12	0.0	NCI-H292 none	4.5
LAK cells IL-2+IFN gamma	0.0	NCI-H292 IL-4	0.0
LAK cells IL-2+ IL-18	0.0	NCI-H292 IL-9	1.5
LAK cells PMA/ionomycin	2.3	NCI-H292 IL-13	0.0
NK Cells IL-2 rest	0.0	NCI-H292 IFN gamma	0.0
Two Way MLR 3 day	1.3	HPAEC none	2.9
Two Way MLR 5 day	0.0	HPAEC TNF alpha + IL-1 beta	2.3
Two Way MLR 7 day	0.9	Lung fibroblast none	5.1
PBMC rest	1.0	Lung fibroblast TNF alpha + IL-1 beta	0.0
PBMC PWM	0.0	Lung fibroblast IL-4	0.0
PBMC PHA-L	0.0	Lung fibroblast IL-9	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-13	0.0
Ramos (B cell) ionomycin	0.0	Lung fibroblast IFN gamma	0.0
B lymphocytes PWM	0.0	Dermal fibroblast CCD1070 rest	9.0
B lymphocytes CD40L and IL-4	0.0	Dermal fibroblast CCD1070 TNF alpha	1.1
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 IL-1 beta	0.0

EOL-1 dbcAMP PMA/ionomycin	0.0	Dermal fibroblast IFN gamma	0.0
Dendritic cells none	2.0	Dermal fibroblast IL-4	2.8
Dendritic cells LPS	17.6	Dermal Fibroblasts rest	0.0
Dendritic cells anti- CD40	2.7	Neutrophils TNFa+LPS	0.0
Monocytes rest	100.0	Neutrophils rest	20.0
Monocytes LPS	6.1	Colon	0.8
Macrophages rest	2.8	Lung	0.0
Macrophages LPS	0.0	Thymus	0.0
HUVEC none	0.0	Kidney	9.3
HUVEC starved	0.0		

CNS_neurodegeneration_v1.0 Summary: Ag3621 Expression of the CG59855-01 gene is low/undetectable in all samples on this panel (CTs>35). (Data not shown.)

General_screening_panel_v1.4 Summary: Ag3621 Expression of the CG59855-01 gene is restricted to samples from fetal lung and adult pancreas (CTs=34.5-35). Thus, expression of this gene can be used to distinguish this sample from other samples in the panel.

The CG59855-01 gene encodes a homologue of ATP synthase subunit c, mitochondrial precursor. Subunit c is an intrinsic membrane component of ATP synthase, and in mammals it is encoded by two expressed nuclear genes, P1 and P2. Both genes encode the same mature c subunit, but the mitochondrial import pre-sequences in the precursors of subunit c are different (ref. 1). Each ATP synthase complex has multiple copies of subunit C. The mitochondrial ATP synthase uses energy derived from a proton gradient to synthesize ATP. The structure of this complex has been referred to as a 'lollipop,' as the soluble F1 catalytic unit is attached to the mitochondrial inner membrane via the F0 unit containing subunit c. F0 subunit C transports protons across the mitochondrial inner membrane to the F1-ATPase (ref. 2).

Subunit C of the Fo region of the ATP synthase complex of the inner mitochondrial membrane is found in high concentrations in lysosomes in late infantile neuronal ceroid lipofuscinosis (Batten's disease). Kominami et al. (1995, Ref 3) found marked delay of degradation of subunit C in patient fibroblasts with no significant differences between control and patient cells with regard to degradation of cytochrome oxidase subunit IV. Furthermore, accumulation of labeled subunit C in the mitochondrial fraction was detected before lysosomal appearance of the radiolabeled subunit, suggesting to the authors a specific failure in the degradation of subunit C after its normal inclusion in mitochondria and its consequent

accumulation in lysosomes. Jolly (1995, ref 4) reported that subunit C represents more than 50% of the accumulated metabolites in the ovine form of the disease and also accumulates significantly in late infantile and juvenile forms of the human disease and several other animal forms. The author suggested that the extreme hydrophobicity and lipophilicity of subunit C may be in part responsible.

References:

1. Dyer MR, Walker JE. (1993) Sequences of members of the human gene family for the c subunit of mitochondrial ATP synthase. *Biochem J* 293 (Pt 1):51-64
2. OMIM 603192
3. Kominami E, Ezaki J, Wolfe LS. (1995) New insight into lysosomal protein storage disease: delayed catabolism of ATP synthase subunit c in Batten disease. *Neurochem Res* 20(11):1305-9
4. Jolly RD. (1995) Batten disease (ceroid-lipofuscinosis): the enigma of subunit c of mitochondrial ATP synthase accumulation. *Neurochem Res* 20(11):1301-4

Panel 4.1D Summary: Ag3621 Expression of the CG59855-01 gene is exclusively seen in resting monocytes (CT=32). Thus, expression of this gene can be used to distinguish this sample from other samples in the panel. In addition, expression of this gene in monocytes suggests a role for the gene product in their function as antigen-presenting cells. This suggests that antibodies or small molecule therapeutics that block the function of this protein may be useful as anti-inflammatory therapeutics for the treatment of autoimmune and inflammatory diseases and for the treatment of immunosuppressed individuals.

DD. CG59807-01: Nuclear Hormone Receptor/Zinc Finger

Expression of gene CG59807-01 was assessed using the primer-probe set Ag3591, described in Table DDA. Results of the RTQ-PCR runs are shown in Tables DDB and DDC.

Table DDA. Probe Name Ag3591

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5' -cactgctccacttttgtcttg-3'	21	1195	728

Probe	TET-5'-cataaaaggacccacacaggagaaaa-3'- TAMRA	26	1216	729
Reverse	5'-cttttccacattcttttgcattc-3'	22	1249	730

Table DDB. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3591, Run 217479278	Tissue Name	Rel. Exp.(%) Ag3591, Run 217479278
Adipose	13.9	Renal ca. TK-10	22.2
Melanoma* Hs688(A).T	18.6	Bladder	27.5
Melanoma* Hs688(B).T	17.6	Gastric ca. (liver met.) NCI-N87	100.0
Melanoma* M14	22.8	Gastric ca. KATO III	63.7
Melanoma* LOXIMVI	12.5	Colon ca. SW-948	4.9
Melanoma* SK- MEL-5	10.4	Colon ca. SW480	41.2
Squamous cell carcinoma SCC-4	27.9	Colon ca.* (SW480 met) SW620	17.1
Testis Pool	14.9	Colon ca. HT29	19.3
Prostate ca.* (bone met) PC-3	51.4	Colon ca. HCT-116	52.9
Prostate Pool	12.7	Colon ca. CaCo-2	13.5
Placenta	8.7	Colon cancer tissue	7.4
Uterus Pool	5.0	Colon ca. SW1116	11.3
Ovarian ca. OVCAR-3	29.9	Colon ca. Colo-205	8.3
Ovarian ca. SK-OV- 3	49.7	Colon ca. SW-48	3.2
Ovarian ca. OVCAR-4	9.1	Colon Pool	18.8
Ovarian ca. OVCAR-5	14.6	Small Intestine Pool	19.2
Ovarian ca. IGROV- 1	26.2	Stomach Pool	15.1
Ovarian ca. OVCAR-8	14.4	Bone Marrow Pool	7.5
Ovary	12.7	Fetal Heart	24.5
Breast ca. MCF-7	9.5	Heart Pool	10.9
Breast ca. MDA- MB-231	42.0	Lymph Node Pool	33.9
Breast ca. BT 549	66.0	Fetal Skeletal Muscle	24.0
Breast ca. T47D	40.3	Skeletal Muscle Pool	19.9

Breast ca. MDA-N	13.7	Spleen Pool	30.4
Breast Pool	25.5	Thymus Pool	30.6
Trachea	14.5	CNS cancer (glio/astro) U87-MG	19.2
Lung	14.6	CNS cancer (glio/astro) U-118-MG	51.1
Fetal Lung	72.7	CNS cancer (neuro;met) SK-N-AS	49.0
Lung ca. NCI-N417	2.6	CNS cancer (astro) SF- 539	18.7
Lung ca. LX-1	21.2	CNS cancer (astro) SNB-75	48.6
Lung ca. NCI-H146	24.5	CNS cancer (glio) SNB-19	26.6
Lung ca. SHP-77	33.7	CNS cancer (glio) SF- 295	80.1
Lung ca. A549	16.6	Brain (Amygdala) Pool	10.6
Lung ca. NCI-H526	14.7	Brain (cerebellum)	65.5
Lung ca. NCI-H23	35.4	Brain (fetal)	50.0
Lung ca. NCI-H460	33.0	Brain (Hippocampus) Pool	15.3
Lung ca. HOP-62	10.4	Cerebral Cortex Pool	18.6
Lung ca. NCI-H522	30.6	Brain (Substantia nigra) Pool	19.9
Liver	2.0	Brain (Thalamus) Pool	26.6
Fetal Liver	21.6	Brain (whole)	25.9
Liver ca. HepG2	16.4	Spinal Cord Pool	16.3
Kidney Pool	27.7	Adrenal Gland	25.0
Fetal Kidney	28.1	Pituitary gland Pool	8.2
Renal ca. 786-0	25.2	Salivary Gland	7.0
Renal ca. A498	12.9	Thyroid (female)	9.2
Renal ca. ACHN	23.5	Pancreatic ca. CAPAN2	12.5
Renal ca. UO-31	32.1	Pancreas Pool	16.8

Table DDC. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag3591, Run 169908857	Tissue Name	Rel. Exp.(%) Ag3591, Run 169908857
Secondary Th1 act	38.4	HUVEC IL-1beta	24.7
Secondary Th2 act	37.4	HUVEC IFN gamma	23.5
Secondary Tr1 act	48.6	HUVEC TNF alpha + IFN gamma	17.3
Secondary Th1 rest	22.7	HUVEC TNF alpha + IL4	20.6

Secondary Th2 rest	34.9	HUVEC IL-11	19.6
Secondary Tr1 rest	35.1	Lung Microvascular EC none	36.6
Primary Th1 act	47.0	Lung Microvascular EC TNFalpha + IL-1beta	39.5
Primary Th2 act	43.5	Microvascular Dermal EC none	22.1
Primary Tr1 act	50.3	Microvascular Dermal EC TNFalpha + IL-1beta	21.9
Primary Th1 rest	43.5	Bronchial epithelium TNFalpha + IL1beta	35.4
Primary Th2 rest	40.6	Small airway epithelium none	14.0
Primary Tr1 rest	51.1	Small airway epithelium TNFalpha + IL-1beta	31.0
CD45RA CD4 lymphocyte act	22.2	Coronary artery SMC rest	14.5
CD45RO CD4 lymphocyte act	38.4	Coronary artery SMC TNFalpha + IL-1beta	12.0
CD8 lymphocyte act	39.8	Astrocytes rest	24.1
Secondary CD8 lymphocyte rest	22.5	Astrocytes TNFalpha + IL-1beta	20.0
Secondary CD8 lymphocyte act	31.0	KU-812 (Basophil) rest	57.8
CD4 lymphocyte none	15.8	KU-812 (Basophil) PMA/ionomycin	98.6
2ry Th1/Th2/Tr1 _anti- CD95 CH11	57.8	CCD1106 (Keratinocytes) none	28.7
LAK cells rest	28.9	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	24.1
LAK cells IL-2	44.4	Liver cirrhosis	8.6
LAK cells IL-2+IL-12	35.4	NCI-H292 none	40.1
LAK cells IL-2+IFN gamma	44.8	NCI-H292 IL-4	80.7
LAK cells IL-2+ IL-18	52.5	NCI-H292 IL-9	79.0
LAK cells PMA/ionomycin	18.3	NCI-H292 IL-13	100.0
NK Cells IL-2 rest	44.1	NCI-H292 IFN gamma	100.0
Two Way MLR 3 day	42.0	HPAEC none	21.6
Two Way MLR 5 day	25.7	HPAEC TNF alpha + IL-1 beta	32.8
Two Way MLR 7 day	20.4	Lung fibroblast none	28.5
PBMC rest	11.2	Lung fibroblast TNF alpha + IL-1 beta	13.9
PBMC PWM	21.3	Lung fibroblast IL-4	28.1

PBMC PHA-L	24.7	Lung fibroblast IL-9	49.3
Ramos (B cell) none	61.1	Lung fibroblast IL-13	37.9
Ramos (B cell) ionomycin	66.9	Lung fibroblast IFN gamma	29.5
B lymphocytes PWM	24.1	Dermal fibroblast CCD1070 rest	29.9
B lymphocytes CD40L and IL-4	56.6	Dermal fibroblast CCD1070 TNF alpha	45.1
EOL-1 dbcAMP	69.7	Dermal fibroblast CCD1070 IL-1 beta	11.0
EOL-1 dbcAMP PMA/ionomycin	54.0	Dermal fibroblast IFN gamma	8.7
Dendritic cells none	26.6	Dermal fibroblast IL-4	29.7
Dendritic cells LPS	10.2	Dermal Fibroblasts rest	12.2
Dendritic cells anti-CD40	23.2	Neutrophils TNFa+LPS	1.3
Monocytes rest	12.2	Neutrophils rest	3.3
Monocytes LPS	16.5	Colon	8.8
Macrophages rest	18.6	Lung	33.4
Macrophages LPS	8.1	Thymus	82.9
HUVEC none	17.4	Kidney	23.8
HUVEC starved	27.2		

General_screening_panel_v1.4 Summary: Ag3591 Highest expression of the CG59807-01 gene is detected in the gastric cancer cell line (CT=28). In addition, high expression of this gene is seen in samples derived from CNS cancer, colon cancer, breast cancer, ovarian cancer, prostate cancer cell lines (CTs=28-31). Therefore, therapeutic modulation of the activity of this gene or its protein product, through the use of small molecule drugs, protein therapeutics or antibodies, might be beneficial in the treatment of these cancers.

In addition, expression of this gene is higher in fetal liver (CT=31) as compared to the corresponding adult tissues (CTs=34). Thus, expression of this gene can be used to distinguish between the fetal and adults source of this tissue.

Among tissues with metabolic or endocrine function, this gene is expressed at high to moderate levels in pancreas, adipose, adrenal gland, thyroid, pituitary gland, skeletal muscle, heart, liver and the gastrointestinal tract. Therefore, therapeutic modulation of the activity of this gene may prove useful in the treatment of endocrine/metabolically related diseases, such as obesity and diabetes.

This gene is also expressed at high levels in all regions of the central nervous system examined, including amygdala, hippocampus, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord. Therefore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

Panel 4.1D Summary: Ag3591 Highest expression of the CG59807-01 gene is detected in treated mucoepidermoid NCI-H292 cells. In addition, this gene is expressed at high to moderate levels in a wide range of cell types of significance in the immune response in health and disease. These cells include members of the T-cell, B-cell, endothelial cell, macrophage/monocyte, and peripheral blood mononuclear cell family, as well as epithelial and fibroblast cell types from lung and skin, and normal tissues represented by colon, lung, thymus and kidney. This ubiquitous pattern of expression suggests that this gene product may be involved in homeostatic processes for these and other cell types and tissues. This pattern is in agreement with the expression profile in General_screening_panel_v1.5 and also suggests a role for the gene product in cell survival and proliferation. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

DE. CG59805-01: Nuclear Hormone Receptor/Zinc Finger

Expression of gene CG59805-01 was assessed using the primer-probe set Ag3590, described in Table DEA. Results of the RTQ-PCR runs are shown in Tables DEB, DEC and DED.

Table DEA. Probe Name Ag3590

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5' -atgagtgcagtgaatgtggaa-3'	21	1620	731
Probe	TET-5' -cttcagtcgcagctcgtccctcact-3' - TAMRA	25	1645	732
Reverse	5' -attctctccagtatgcattcctt-3'	22	1678	733

Table DEB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3590, Run 211006692	Tissue Name	Rel. Exp.(%) Ag3590, Run 211006692
AD 1 Hippo	16.7	Control (Path) 3 Temporal Ctx	5.8
AD 2 Hippo	22.1	Control (Path) 4 Temporal Ctx	42.6
AD 3 Hippo	8.2	AD 1 Occipital Ctx	17.7
AD 4 Hippo	7.9	AD 2 Occipital Ctx (Missing)	0.0
AD 5 Hippo	73.2	AD 3 Occipital Ctx	3.9
AD 6 Hippo	87.7	AD 4 Occipital Ctx	23.3
Control 2 Hippo	25.7	AD 5 Occipital Ctx	32.5
Control 4 Hippo	17.0	AD 6 Occipital Ctx	31.2
Control (Path) 3 Hippo	7.4	Control 1 Occipital Ctx	5.2
AD 1 Temporal Ctx	25.2	Control 2 Occipital Ctx	39.2
AD 2 Temporal Ctx	34.2	Control 3 Occipital Ctx	20.0
AD 3 Temporal Ctx	10.1	Control 4 Occipital Ctx	8.1
AD 4 Temporal Ctx	28.3	Control (Path) 1 Occipital Ctx	80.7
AD 5 Inf Temporal Ctx	71.7	Control (Path) 2 Occipital Ctx	11.1
AD 5 Sup Temporal Ctx	35.4	Control (Path) 3 Occipital Ctx	6.1
AD 6 Inf Temporal Ctx	98.6	Control (Path) 4 Occipital Ctx	17.9
AD 6 Sup Temporal Ctx	100.0	Control 1 Parietal Ctx	8.8
Control 1 Temporal Ctx	8.2	Control 2 Parietal Ctx	39.0
Control 2 Temporal Ctx	29.1	Control 3 Parietal Ctx	18.3
Control 3 Temporal Ctx	17.3	Control (Path) 1 Parietal Ctx	55.5
Control 3 Temporal Ctx	10.2	Control (Path) 2 Parietal Ctx	26.8
Control (Path) 1 Temporal Ctx	50.7	Control (Path) 3 Parietal Ctx	7.4
Control (Path) 2 Temporal Ctx	34.6	Control (Path) 4 Parietal Ctx	46.0

Table DEC. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3590, Run 217474417	Tissue Name	Rel. Exp.(%) Ag3590, Run 217474417
Adipose	12.8	Renal ca. TK-10	28.9
Melanoma* Hs688(A).T	33.7	Bladder	28.5
Melanoma* Hs688(B).T	25.3	Gastric ca. (liver met.) NCI-N87	82.4
Melanoma* M14	16.3	Gastric ca. KATO III	24.5
Melanoma* LOXIMVI	19.6	Colon ca. SW-948	5.8
Melanoma* SK- MEL-5	16.5	Colon ca. SW480	28.1
Squamous cell carcinoma SCC-4	29.5	Colon ca. * (SW480 met) SW620	10.7
Testis Pool	16.0	Colon ca. HT29	13.6
Prostate ca.* (bone met) PC-3	57.4	Colon ca. HCT-116	26.2
Prostate Pool	14.6	Colon ca. CaCo-2	28.5
Placenta	7.7	Colon cancer tissue	13.0
Uterus Pool	6.0	Colon ca. SW1116	4.8
Ovarian ca. OVCAR-3	18.9	Colon ca. Colo-205	3.4
Ovarian ca. SK-OV- 3	38.2	Colon ca. SW-48	2.3
Ovarian ca. OVCAR-4	15.4	Colon Pool	27.0
Ovarian ca. OVCAR-5	17.4	Small Intestine Pool	24.1
Ovarian ca. IGROV- 1	12.2	Stomach Pool	14.3
Ovarian ca. OVCAR-8	12.5	Bone Marrow Pool	11.7
Ovary	14.2	Fetal Heart	21.8
Breast ca. MCF-7	29.1	Heart Pool	10.7
Breast ca. MDA- MB-231	28.3	Lymph Node Pool	29.5
Breast ca. BT 549	100.0	Fetal Skeletal Muscle	10.7
Breast ca. T47D	34.4	Skeletal Muscle Pool	14.7
Breast ca. MDA-N	12.5	Spleen Pool	26.2
Breast Pool	40.6	Thymus Pool	26.8
Trachea	16.3	CNS cancer (glio/astro) U87-MG	32.3
Lung	4.6	CNS cancer (glio/astro) U-118-MG	57.0

Fetal Lung	66.4	CNS cancer (neuro;met) SK-N-AS	33.2
Lung ca. NCI-N417	2.0	CNS cancer (astro) SF-539	14.4
Lung ca. LX-1	15.9	CNS cancer (astro) SNB-75	46.7
Lung ca. NCI-H146	3.3	CNS cancer (glio) SNB-19	14.9
Lung ca. SHP-77	24.5	CNS cancer (glio) SF-295	82.9
Lung ca. A549	17.2	Brain (Amygdala) Pool	7.2
Lung ca. NCI-H526	5.4	Brain (cerebellum)	13.2
Lung ca. NCI-H23	26.4	Brain (fetal)	26.8
Lung ca. NCI-H460	22.5	Brain (Hippocampus) Pool	10.3
Lung ca. HOP-62	10.6	Cerebral Cortex Pool	14.6
Lung ca. NCI-H522	18.9	Brain (Substantia nigra) Pool	13.9
Liver	1.6	Brain (Thalamus) Pool	18.2
Fetal Liver	26.1	Brain (whole)	16.5
Liver ca. HepG2	19.8	Spinal Cord Pool	9.1
Kidney Pool	43.5	Adrenal Gland	30.8
Fetal Kidney	26.2	Pituitary gland Pool	7.3
Renal ca. 786-0	26.1	Salivary Gland	7.7
Renal ca. A498	19.8	Thyroid (female)	6.5
Renal ca. ACHN	14.6	Pancreatic ca. CAPAN2	13.3
Renal ca. UO-31	27.0	Pancreas Pool	25.2

Table DED. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag3590, Run 169908854	Tissue Name	Rel. Exp.(%) Ag3590, Run 169908854
Secondary Th1 act	33.9	HUVEC IL-1beta	31.0
Secondary Th2 act	42.6	HUVEC IFN gamma	30.6
Secondary Tr1 act	52.1	HUVEC TNF alpha + IFN gamma	18.9
Secondary Th1 rest	20.3	HUVEC TNF alpha + IL4	18.2
Secondary Th2 rest	28.1	HUVEC IL-11	17.4
Secondary Tr1 rest	26.6	Lung Microvascular EC none	39.5
Primary Th1 act	44.1	Lung Microvascular EC TNFalpha + IL-1beta	54.0
Primary Th2 act	38.7	Microvascular Dermal EC	25.9

		none	
Primary Tr1 act	45.7	Microsvascular Dermal EC TNFalpha + IL-1beta	36.6
Primary Th1 rest	23.3	Bronchial epithelium TNFalpha + IL1beta	51.1
Primary Th2 rest	27.7	Small airway epithelium none	22.1
Primary Tr1 rest	30.4	Small airway epithelium TNFalpha + IL-1beta	33.0
CD45RA CD4 lymphocyte act	24.8	Coronary artery SMC rest	38.4
CD45RO CD4 lymphocyte act	42.9	Coronary artery SMC TNFalpha + IL-1beta	29.1
CD8 lymphocyte act	39.2	Astrocytes rest	34.9
Secondary CD8 lymphocyte rest	32.8	Astrocytes TNFalpha + IL-1beta	26.2
Secondary CD8 lymphocyte act	19.5	KU-812 (Basophil) rest	56.6
CD4 lymphocyte none	37.4	KU-812 (Basophil) PMA/ionomycin	100.0
2ry Th1/Th2/Tr1 _anti- CD95 CH11	39.8	CCD1106 (Keratinocytes) none	29.3
LAK cells rest	43.8	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	34.9
LAK cells IL-2	38.2	Liver cirrhosis	12.9
LAK cells IL-2+IL-12	39.5	NCI-H292 none	22.2
LAK cells IL-2+IFN gamma	50.3	NCI-H292 IL-4	38.7
LAK cells IL-2+ IL-18	51.1	NCI-H292 IL-9	41.2
LAK cells PMA/ionomycin	50.0	NCI-H292 IL-13	36.1
NK Cells IL-2 rest	41.5	NCI-H292 IFN gamma	56.3
Two Way MLR 3 day	50.7	HPAEC none	19.3
Two Way MLR 5 day	28.5	HPAEC TNF alpha + IL-1 beta	50.3
Two Way MLR 7 day	19.5	Lung fibroblast none	37.6
PBMC rest	33.2	Lung fibroblast TNF alpha + IL-1 beta	24.0
PBMC PWM	25.7	Lung fibroblast IL-4	49.3
PBMC PHA-L	16.3	Lung fibroblast IL-9	56.6
Ramos (B cell) none	42.3	Lung fibroblast IL-13	43.5
Ramos (B cell) ionomycin	33.4	Lung fibroblast IFN gamma	42.9
B lymphocytes PWM	24.3	Dermal fibroblast CCD1070 rest	38.7

B lymphocytes CD40L and IL-4	36.9	Dermal fibroblast CCD1070 TNF alpha	43.8
EOL-1 dbcAMP	40.3	Dermal fibroblast CCD1070 IL-1 beta	22.8
EOL-1 dbcAMP PMA/ionomycin	37.9	Dermal fibroblast IFN gamma	12.3
Dendritic cells none	33.7	Dermal fibroblast IL-4	55.1
Dendritic cells LPS	18.9	Dermal Fibroblasts rest	23.2
Dendritic cells anti-CD40	26.8	Neutrophils TNFa+LPS	1.4
Monocytes rest	33.7	Neutrophils rest	16.5
Monocytes LPS	31.4	Colon	8.8
Macrophages rest	19.8	Lung	41.2
Macrophages LPS	6.6	Thymus	82.9
HUVEC none	16.0	Kidney	30.8
HUVEC starved	20.0		

CNS_neurodegeneration_v1.0 Summary: Ag3590 This panel confirms the expression of the CG59805-01 gene at low levels in the brain in an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. Please see Panel 1.4 for a discussion of the potential utility of this gene in treatment of central nervous system disorders.

General_screening_panel_v1.4 Summary: Ag3590 Highest expression of the CG59805-01 gene is detected in one of the breast cancer cell line BT 549 (CT=26). In addition, expression of this gene is high in CNS cancer, gastric cancer, and prostate cancer cell lines. Therefore, expression of this gene can be used to distinguish these samples from other samples in this panel and it can be used as marker for detection of these cancers. Furthermore, therapeutic modulation of the activity of the protein encoded by this gene may be beneficial in the treatment of these cancers.

Among tissues with metabolic or endocrine function, this gene is expressed at high to moderate levels in pancreas, adipose, adrenal gland, thyroid, pituitary gland, skeletal muscle, heart, liver and the gastrointestinal tract. Therefore, therapeutic modulation of the activity of this gene may prove useful in the treatment of endocrine/metabolically related diseases, such as obesity and diabetes.

In addition, this gene is expressed at high levels in all regions of the central nervous system examined, including amygdala, hippocampus, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord. Therefore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

Panel 4.1D Summary: Ag3590 Highest expression of the CG59805-01 gene is detected in PMA/ionomycin treated Ku-812 (basophil) cells (CT=29). In addition, this gene is expressed at high to moderate levels in a wide range of cell types of significance in the immune response in health and disease. These cells include members of the T-cell, B-cell, endothelial cell, macrophage/monocyte, and peripheral blood mononuclear cell family, as well as epithelial and fibroblast cell types from lung and skin, and normal tissues represented by colon, lung, thymus and kidney. This ubiquitous pattern of expression suggests that this gene product may be involved in homeostatic processes for these and other cell types and tissues. This pattern is in agreement with the expression profile in General_screening_panel_v1.4 and also suggests a role for the gene product in cell survival and proliferation. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

DF. CG59928-01: Novel Universal Stress (USP) Domain Containg Protein

Expression of gene CG59928-01 was assessed using the primer-probe set Ag3636, described in Table DFA. Please note that this sequence is represented by a full length clone.

Table DFA. Probe Name Ag3636

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-gaagccttcgacaagctgat-3'	20	1268	734
Probe	TET-5'-atcgatagagcacaggcccacctggtt-3'-TAMRA	26	1301	735
Reverse	5'-gatgacttctcgcgcaaaac-3'	20	1332	736

CNS_neurodegeneration_v1.0 Summary: Ag3636 Expression of the CG59928-01 gene is low/undetectable in all samples on this panel (CTs>35). (Data not shown.) The amp plot indicates that there is a high probability of a probe failure.

General_screening_panel_v1.4 Summary: Ag3636 Expression of the CG59928-01 gene is low/undetectable in all samples on this panel (CTs>35). (Data not shown.) The amp plot indicates that there is a high probability of a probe failure.

Panel 4.1D Summary: Ag3636 Expression of the CG59928-01 gene is low/undetectable in all samples on this panel (CTs>35). (Data not shown.) The amp plot indicates that there is a high probability of a probe failure.

DG. CG59947-01: VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3

Expression of gene CG59947-01 was assessed using the primer-probe set Ag3635, described in Table DGA. Results of the RTQ-PCR runs are shown in Tables DGB, DGC, DGD and DGE.

Table DGA. Probe Name Ag3635

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-tacttcaagaacatccccattg-3'	22	1326	737
Probe	TET-5'-ctgtgggtcaccatgacgacctg-3'-TAMRA	23	1360	738
Reverse	5'-tcttggggtacatgtctccata-3'	22	1386	739

Table DGB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3635, Run 211020704	Tissue Name	Rel. Exp.(%) Ag3635, Run 211020704
AD 1 Hippo	8.7	Control (Path) 3 Temporal Ctx	2.8
AD 2 Hippo	14.3	Control (Path) 4 Temporal Ctx	23.8
AD 3 Hippo	5.1	AD 1 Occipital Ctx	0.9
AD 4 Hippo	4.8	AD 2 Occipital Ctx (Missing)	0.0
AD 5 hippo	100.0	AD 3 Occipital Ctx	4.2
AD 6 Hippo	23.7	AD 4 Occipital Ctx	13.0
Control 2 Hippo	22.4	AD 5 Occipital Ctx	18.4
Control 4 Hippo	4.9	AD 6 Occipital Ctx	47.3
Control (Path) 3 Hippo	2.7	Control 1 Occipital Ctx	2.0
AD 1 Temporal Ctx	6.8	Control 2 Occipital	99.3

		Ctx	
AD 2 Temporal Ctx	18.3	Control 3 Occipital Ctx	11.3
AD 3 Temporal Ctx	4.6	Control 4 Occipital Ctx	2.6
AD 4 Temporal Ctx	11.5	Control (Path) 1 Occipital Ctx	80.7
AD 5 Inf Temporal Ctx	68.8	Control (Path) 2 Occipital Ctx	10.4
AD 5 Sup Temporal Ctx	23.5	Control (Path) 3 Occipital Ctx	2.5
AD 6 Inf Temporal Ctx	21.6	Control (Path) 4 Occipital Ctx	18.4
AD 6 Sup Temporal Ctx	31.0	Control 1 Parietal Ctx	3.9
Control 1 Temporal Ctx	3.8	Control 2 Parietal Ctx	20.2
Control 2 Temporal Ctx	30.8	Control 3 Parietal Ctx	20.3
Control 3 Temporal Ctx	8.3	Control (Path) 1 Parietal Ctx	66.4
Control 4 Temporal Ctx	4.9	Control (Path) 2 Parietal Ctx	21.2
Control (Path) 1 Temporal Ctx	46.7	Control (Path) 3 Parietal Ctx	1.8
Control (Path) 2 Temporal Ctx	16.8	Control (Path) 4 Parietal Ctx	51.4

Table DGC. Panel 2.2

Tissue Name	Rel. Exp.(%) Ag3635, Run 173764364	Tissue Name	Rel. Exp.(%) Ag3635, Run 173764364
Normal Colon	5.4	Kidney Margin (OD04348)	100.0
Colon cancer (OD06064)	5.0	Kidney malignant cancer (OD06204B)	5.0
Colon Margin (OD06064)	3.0	Kidney normal adjacent tissue (OD06204E)	19.2
Colon cancer (OD06159)	1.0	Kidney Cancer (OD04450-01)	5.7
Colon Margin (OD06159)	2.8	Kidney Margin (OD04450-03)	23.3
Colon cancer (OD06297-04)	2.0	Kidney Cancer 8120613	1.2

Colon Margin (OD06297-05)	5.0	Kidney Margin 8120614	23.5
CC Gr.2 ascend colon (ODO3921)	4.4	Kidney Cancer 9010320	3.6
CC Margin (ODO3921)	0.7	Kidney Margin 9010321	12.9
Colon cancer metastasis (OD06104)	1.8	Kidney Cancer 8120607	13.3
Lung Margin (OD06104)	0.6	Kidney Margin 8120608	16.3
Colon mets to lung (OD04451-01)	1.6	Normal Uterus	6.3
Lung Margin (OD04451-02)	6.1	Uterine Cancer 064011	20.3
Normal Prostate	8.2	Normal Thyroid	6.7
Prostate Cancer (OD04410)	2.2	Thyroid Cancer 064010	4.8
Prostate Margin (OD04410)	3.4	Thyroid Cancer A302152	33.7
Normal Ovary	5.4	Thyroid Margin A302153	7.0
Ovarian cancer (OD06283-03)	9.9	Normal Breast	23.7
Ovarian Margin (OD06283-07)	5.6	Breast Cancer (OD04566)	3.2
Ovarian Cancer 064008	8.0	Breast Cancer 1024	63.3
Ovarian cancer (OD06145)	13.1	Breast Cancer (OD04590-01)	8.7
Ovarian Margin (OD06145)	15.7	Breast Cancer Mets (OD04590-03)	4.0
Ovarian cancer (OD06455-03)	24.7	Breast Cancer Metastasis (OD04655- 05)	78.5
Ovarian Margin (OD06455-07)	3.5	Breast Cancer 064006	16.3
Normal Lung	8.2	Breast Cancer 9100266	5.2
Invasive poor diff. lung adeno (ODO4945-01)	5.4	Breast Margin 9100265	5.4
Lung Margin (ODO4945-03)	7.7	Breast Cancer A209073	2.2
Lung Malignant Cancer (OD03126)	3.7	Breast Margin A2090734	20.3
Lung Margin (OD03126)	3.1	Breast cancer (OD06083)	9.1
Lung Cancer	8.8	Breast cancer node	7.6

(OD05014A)		metastasis (OD06083)	
Lung Margin (OD05014B)	12.6	Normal Liver	7.4
Lung cancer (OD06081)	11.0	Liver Cancer 1026	4.5
Lung Margin (OD06081)	6.7	Liver Cancer 1025	9.7
Lung Cancer (OD04237-01)	1.0	Liver Cancer 6004-T	7.4
Lung Margin (OD04237-02)	10.4	Liver Tissue 6004-N	7.4
Ocular Melanoma Metastasis	5.1	Liver Cancer 6005-T	5.2
Ocular Melanoma Margin (Liver)	6.1	Liver Tissue 6005-N	8.8
Melanoma Metastasis	1.6	Liver Cancer 064003	5.9
Melanoma Margin (Lung)	5.1	Normal Bladder	6.1
Normal Kidney	11.3	Bladder Cancer 1023	4.6
Kidney Ca, Nuclear grade 2 (OD04338)	51.8	Bladder Cancer A302173	7.9
Kidney Margin (OD04338)	4.7	Normal Stomach	8.6
Kidney Ca Nuclear grade 1/2 (OD04339)	24.5	Gastric Cancer 9060397	1.2
Kidney Margin (OD04339)	21.5	Stomach Margin 9060396	4.3
Kidney Ca, Clear cell type (OD04340)	2.3	Gastric Cancer 9060395	1.9
Kidney Margin (OD04340)	14.8	Stomach Margin 9060394	6.8
Kidney Ca, Nuclear grade 3 (OD04348)	1.1	Gastric Cancer 064005	3.1

Table DGD. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag3635, Run 169960385	Tissue Name	Rel. Exp.(%) Ag3635, Run 169960385
Secondary Th1 act	26.1	HUVEC IL-1beta	12.5
Secondary Th2 act	19.1	HUVEC IFN gamma	34.6
Secondary Tr1 act	12.7	HUVEC TNF alpha + IFN gamma	3.2
Secondary Th1 rest	2.0	HUVEC TNF alpha + IL4	5.3
Secondary Th2 rest	8.2	HUVEC IL-11	29.3
Secondary Tr1 rest	4.8	Lung Microvascular EC	12.7

		none	
Primary Th1 act	16.0	Lung Microvascular EC TNFalpha + IL-1beta	3.0
Primary Th2 act	17.8	Microvascular Dermal EC none	6.0
Primary Tr1 act	13.1	Microvascular Dermal EC TNFalpha + IL-1beta	4.3
Primary Th1 rest	3.4	Bronchial epithelium TNFalpha + IL1beta	12.5
Primary Th2 rest	6.3	Small airway epithelium none	4.5
Primary Tr1 rest	5.4	Small airway epithelium TNFalpha + IL-1beta	11.0
CD45RA CD4 lymphocyte act	17.1	Coronary artery SMC rest	20.4
CD45RO CD4 lymphocyte act	44.1	Coronary artery SMC TNFalpha + IL-1beta	21.8
CD8 lymphocyte act	23.3	Astrocytes rest	6.4
Secondary CD8 lymphocyte rest	42.9	Astrocytes TNFalpha + IL-1beta	9.9
Secondary CD8 lymphocyte act	7.4	KU-812 (Basophil) rest	0.2
CD4 lymphocyte none	11.5	KU-812 (Basophil) PMA/ionomycin	0.8
2ry Th1/Th2/Tr1_anti- CD95 CH11	2.4	CCD1106 (Keratinocytes) none	11.2
LAK cells rest	36.3	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	22.8
LAK cells IL-2	9.1	Liver cirrhosis	7.4
LAK cells IL-2+IL-12	22.8	NCI-H292 none	14.3
LAK cells IL-2+IFN gamma	21.8	NCI-H292 IL-4	20.9
LAK cells IL-2+ IL-18	21.2	NCI-H292 IL-9	26.1
LAK cells PMA/ionomycin	21.0	NCI-H292 IL-13	25.5
NK Cells IL-2 rest	8.7	NCI-H292 IFN gamma	13.2
Two Way MLR 3 day	24.8	HPAEC none	32.5
Two Way MLR 5 day	18.7	HPAEC TNF alpha + IL-1 beta	14.3
Two Way MLR 7 day	21.6	Lung fibroblast none	1.3
PBMC rest	23.0	Lung fibroblast TNF alpha + IL-1 beta	0.8
PBMC PWM	71.2	Lung fibroblast IL-4	1.5
PBMC PHA-L	46.7	Lung fibroblast IL-9	2.9
Ramos (B cell) none	1.8	Lung fibroblast IL-13	1.4

Ramos (B cell) ionomycin	1.5	Lung fibroblast IFN gamma	1.2
B lymphocytes PWM	49.7	Dermal fibroblast CCD1070 rest	33.7
B lymphocytes CD40L and IL-4	68.8	Dermal fibroblast CCD1070 TNF alpha	22.5
EOL-1 dbcAMP	22.7	Dermal fibroblast CCD1070 IL-1 beta	10.1
EOL-1 dbcAMP PMA/ionomycin	40.3	Dermal fibroblast IFN gamma	6.1
Dendritic cells none	54.0	Dermal fibroblast IL-4	10.4
Dendritic cells LPS	73.7	Dermal Fibroblasts rest	9.9
Dendritic cells anti- CD40	100.0	Neutrophils TNFa+LPS	0.8
Monocytes rest	66.0	Neutrophils rest	2.8
Monocytes LPS	22.4	Colon	6.7
Macrophages rest	86.5	Lung	34.6
Macrophages LPS	13.4	Thymus	51.1
HUVEC none	8.6	Kidney	90.8
HUVEC starved	11.3		

Table DGE. Panel CNS_1

Tissue Name	Rel. Exp.(%) Ag3635, Run 171648701	Tissue Name	Rel. Exp.(%) Ag3635, Run 171648701
BA4 Control	16.7	BA17 PSP	27.0
BA4 Control2	39.2	BA17 PSP2	8.9
BA4 Alzheimer's2	5.0	Sub Nigra Control	1.1
BA4 Parkinson's	28.5	Sub Nigra Control2	16.5
BA4 Parkinson's2	100.0	Sub Nigra Alzheimer's2	4.1
BA4 Huntington's	24.7	Sub Nigra Parkinson's2	26.1
BA4 Huntington's2	9.7	Sub Nigra Huntington's	25.3
BA4 PSP	11.7	Sub Nigra Huntington's2	9.3
BA4 PSP2	36.6	Sub Nigra PSP2	2.4
BA4 Depression	14.9	Sub Nigra Depression	2.0
BA4 Depression2	8.8	Sub Nigra Depression2	4.5
BA7 Control	25.3	Glob Palladus	3.3

		Control	
BA7 Control2	42.6	Glob Palladus Control2	4.9
BA7 Alzheimer's2	4.5	Glob Palladus Alzheimer's	4.5
BA7 Parkinson's	10.4	Glob Palladus Alzheimer's2	1.2
BA7 Parkinson's2	29.5	Glob Palladus Parkinson's	21.6
BA7 Huntington's	25.3	Glob Palladus Parkinson's2	2.0
BA7 Huntington's2	12.9	Glob Palladus PSP	1.6
BA7 PSP	30.6	Glob Palladus PSP2	2.1
BA7 PSP2	12.1	Glob Palladus Depression	1.4
BA7 Depression	10.1	Temp Pole Control	7.3
BA9 Control	15.0	Temp Pole Control2	27.4
BA9 Control2	47.0	Temp Pole Alzheimer's	4.2
BA9 Alzheimer's	4.7	Temp Pole Alzheimer's2	2.5
BA9 Alzheimer's2	9.2	Temp Pole Parkinson's	15.1
BA9 Parkinson's	28.9	Temp Pole Parkinson's2	14.2
BA9 Parkinson's2	34.4	Temp Pole Huntington's	19.2
BA9 Huntington's	24.1	Temp Pole PSP	3.4
BA9 Huntington's2	9.5	Temp Pole PSP2	3.0
BA9 PSP	10.2	Temp Pole Depression2	4.8
BA9 PSP2	6.2	Cing Gyr Control	20.9
BA9 Depression	5.6	Cing Gyr Control2	25.9
BA9 Depression2	8.3	Cing Gyr Alzheimer's	5.6
BA17 Control	33.2	Cing Gyr Alzheimer's2	6.3
BA17 Control2	64.6	Cing Gyr Parkinson's	9.1
BA17 Alzheimer's2	7.2	Cing Gyr Parkinson's2	13.1
BA17 Parkinson's	18.3	Cing Gyr Huntington's	22.1

BA17 Parkinson's2	35.1	Cing Gyr Huntington's2	6.0
BA17 Huntington's	32.1	Cing Gyr PSP	6.5
BA17 Huntington's2	8.8	Cing Gyr PSP2	2.6
BA17 Depression	7.3	Cing Gyr Depression	2.6
BA17 Depression2	25.7	Cing Gyr Depression2	6.1

CNS_neurodegeneration_v1.0 Summary: Ag3635 This panel confirms the expression of CG59947-01 gene at low levels in the brain in an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. This gene encodes a potassium channel protein homolog. The significant levels of expression in the brain may indicate a role for this protein in signal processing in the central nervous system.

References:

1. Rudy B, Chow A, Lau D, Amarillo Y, Ozaita A, Saganich M, Moreno H, Nadal MS, Hernandez-Pineda R, Hernandez-Cruz A, Erisir A, Leonard C, Vega-Saenz de Miera E.
2. Contributions of Kv3 channels to neuronal excitability. Ann N Y Acad Sci 1999 Apr 30;868:304-43

General_screening_panel_v1.4 Summary: Ag3635 Results from one experiment with the CG59947-01 gene are not included. The amp plot indicates that there were experimental difficulties with this run.

Panel 2.2 Summary: Ag3635 Highest expression of the CG59447-01 gene is seen in normal kidney tissue adjacent to a tumor (CT=28). In addition, expression appears to be higher in normal kidney tissue than in the adjacent tumor in six out of nine matched pairs. Conversely expression appears to be higher in breast cancer than in matched normal breast tissue. Thus, expression of this gene could be used to differentiate between these samples and other samples on this panel and as a marker for kidney and breast cancers. Furthermore, therapeutic modulation of the expression or function of this protein may be effective in the treatment of breast and kidney cancer.

Panel 4.1D Summary: Ag3635 This gene is expressed at high to moderate levels in a wide range of cell types of significance in the immune response in health and disease, with highest expression in anti CD40 dendritic cells (CT=28.1). Other cells that express this protein include members of the T-cell, B-cell, endothelial cell, macrophage/monocyte, and peripheral blood mononuclear cell family, as well as epithelial and fibroblast cell types from lung and skin, and normal tissues represented by colon, lung, thymus and kidney. This ubiquitous pattern of expression suggests that this gene product may be involved in homeostatic processes for these and other cell types and tissues. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

Panel CNS_1 Summary: Ag3635 Expression in this panel confirms expression of the CG59947-01 gene in the brain. Please see Panel CNS_neurodegeneration_v1.0 for discussion of utility of this gene in the central nervous system.

DH. CG59938-01: arylsulfatase

Expression of gene CG59938-01 was assessed using the primer-probe set Ag3634, described in Table DHA.

Table DHA. Probe Name Ag3634

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-agccaatgaaaggagagaaagt-3'	22	870	740
Probe	TET-5'-cttcctcatgctgaaggaggcactt-3'- TAMRA	26	894	741
Reverse	5'-cccttttgtagctttcaatgaa-3'	22	923	742

CNS_neurodegeneration_v1.0 Summary: Ag3634 Expression of the CG59938-01 gene is low/undetectable in all samples on this panel (CTs>35). (Data not shown.)

General_screening_panel_v1.4 Summary: Ag3634 Expression of the CG59938-01 gene is low/undetectable in all samples on this panel (CTs>35). (Data not shown.)

Panel 2.2 Summary: Ag3634 Expression of the CG59938-01 gene is low/undetectable in all samples on this panel (CTs>35). (Data not shown.)

Panel 4.1D Summary: Ag3634 Expression of the CG55938-01 gene is low/undetectable in all samples on this panel (CTs>35). (Data not shown.)

DI. CG59746-01: Ubiquitin Carboxyl-terminal Hydrolase

Expression of gene CG59746-01 was assessed using the primer-probe set Ag3574, described in Table DIA.

Table DIA. Probe Name Ag3574

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5' - agcacaacacagaaggaaatca - 3'	22	461	743
Probe	TET-5' - tcattccacaaagttgatgagaaatca - 3' - TAMRA	27	491	744
Reverse	5' - gtcccacttccttttgcatact - 3'	22	534	745

CNS_neurodegeneration_v1.0 Summary: Ag3574 Expression of the CG59746-01 gene is low/undetectable in all samples on this panel (CTs>35). (Data not shown.)

General_screening_panel_v1.4 Summary: Ag3574 Expression of the CG59746-01 gene is low/undetectable in all samples on this panel (CTs>35). (Data not shown.)

Panel 2.2 Summary: Ag3574 Expression of the CG59746-01 gene is low/undetectable in all samples on this panel (CTs>35). (Data not shown.)

Panel 4.1D Summary: Ag3574 Expression of the CG59746-01 gene is low/undetectable in all samples on this panel (CTs>35). (Data not shown.)

Panel CNS_1 Summary: Ag3574 Expression of the CG59746-01 gene is low/undetectable in all samples on this panel (CTs>35). (Data not shown.)

DJ. CG88613-01: INOSITOL 1,4,5-TRISPHOSPHATE 3-KINASE ISOENZYME

Expression of gene CG88613-01 was assessed using the primer-probe set Ag3647, described in Table DJA. Results of the RTQ-PCR runs are shown in Tables DJB, DJC and DJD.

Table DJA. Probe Name Ag3647

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5' - actggagcaggtgacaaaagt - 3'	21	1731	766
Probe	TET-5' - accacgtcatcctgcaaaagtacgtg - 3' - TAMRA	26	1775	767
Reverse	5' - cagagcttcacgaagttcttct - 3'	22	1809	768

Table DJB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3647, Run 211019283	Tissue Name	Rel. Exp.(%) Ag3647, Run 211019283
AD 1 Hippo	44.8	Control (Path) 3 Temporal Ctx	16.3
AD 2 Hippo	28.1	Control (Path) 4 Temporal Ctx	20.7
AD 3 Hippo	10.2	AD 1 Occipital Ctx	30.1
AD 4 Hippo	10.7	AD 2 Occipital Ctx (Missing)	0.0
AD 5 hippo	98.6	AD 3 Occipital Ctx	17.1
AD 6 Hippo	75.3	AD 4 Occipital Ctx	17.9
Control 2 Hippo	33.4	AD 5 Occipital Ctx	39.8
Control 4 Hippo	29.1	AD 6 Occipital Ctx	42.6
Control (Path) 3 Hippo	14.9	Control 1 Occipital Ctx	8.0
AD 1 Temporal Ctx	19.5	Control 2 Occipital Ctx	67.4
AD 2 Temporal Ctx	29.1	Control 3 Occipital Ctx	29.3
AD 3 Temporal Ctx	14.2	Control 4 Occipital Ctx	16.6
AD 4 Temporal Ctx	23.8	Control (Path) 1 Occipital Ctx	57.4
AD 5 Inf Temporal Ctx	100.0	Control (Path) 2 Occipital Ctx	12.9
AD 5 SupTemporal Ctx	69.7	Control (Path) 3 Occipital Ctx	14.6
AD 6 Inf Temporal Ctx	73.2	Control (Path) 4 Occipital Ctx	12.5
AD 6 Sup Temporal Ctx	57.8	Control 1 Parietal Ctx	11.7
Control 1 Temporal Ctx	17.3	Control 2 Parietal Ctx	50.0
Control 2 Temporal Ctx	47.6	Control 3 Parietal Ctx	39.0
Control 3 Temporal	32.5	Control (Path) 1	41.8

Ctx		Parietal Ctx	
Control 4 Temporal Ctx	20.9	Control (Path) 2 Parietal Ctx	18.4
Control (Path) 1 Temporal Ctx	35.6	Control (Path) 3 Parietal Ctx	16.0
Control (Path) 2 Temporal Ctx	28.3	Control (Path) 4 Parietal Ctx	20.4

Table DJC. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3647, Run 218342103	Tissue Name	Rel. Exp.(%) Ag3647, Run 218342103
Adipose	37.9	Renal ca. TK-10	23.3
Melanoma* Hs688(A).T	15.7	Bladder	24.1
Melanoma* Hs688(B).T	20.2	Gastric ca. (liver met.) NCI-N87	100.0
Melanoma* M14	11.3	Gastric ca. KATO III	25.2
Melanoma* LOXIMVI	8.5	Colon ca. SW-948	11.2
Melanoma* SK- MEL-5	13.0	Colon ca. SW480	38.7
Squamous cell carcinoma SCC-4	35.6	Colon ca.* (SW480 met) SW620	11.7
Testis Pool	6.4	Colon ca. HT29	17.2
Prostate ca.* (bone met) PC-3	11.7	Colon ca. HCT-116	24.1
Prostate Pool	12.7	Colon ca. CaCo-2	78.5
Placenta	31.6	Colon cancer tissue	37.1
Uterus Pool	4.5	Colon ca. SW1116	8.0
Ovarian ca. OVCAR-3	21.2	Colon ca. Colo-205	4.6
Ovarian ca. SK-OV- 3	22.2	Colon ca. SW-48	9.3
Ovarian ca. OVCAR-4	22.2	Colon Pool	13.5
Ovarian ca. OVCAR-5	32.5	Small Intestine Pool	13.0
Ovarian ca. IGROV- 1	32.8	Stomach Pool	11.7
Ovarian ca. OVCAR-8	14.3	Bone Marrow Pool	5.7
Ovary	7.9	Fetal Heart	5.0
Breast ca. MCF-7	50.0	Heart Pool	6.4

Breast ca. MDA-MB-231	25.7	Lymph Node Pool	11.2
Breast ca. BT 549	61.1	Fetal Skeletal Muscle	4.4
Breast ca. T47D	87.7	Skeletal Muscle Pool	11.6
Breast ca. MDA-N	7.4	Spleen Pool	6.0
Breast Pool	10.6	Thymus Pool	8.3
Trachea	24.5	CNS cancer (glio/astro) U87-MG	14.9
Lung	3.5	CNS cancer (glio/astro) U-118-MG	16.6
Fetal Lung	95.3	CNS cancer (neuro;met) SK-N-AS	15.7
Lung ca. NCI-N417	3.9	CNS cancer (astro) SF-539	11.3
Lung ca. LX-1	16.4	CNS cancer (astro) SNB-75	34.4
Lung ca. NCI-H146	6.0	CNS cancer (glio) SNB-19	48.0
Lung ca. SHP-77	23.3	CNS cancer (glio) SF-295	45.4
Lung ca. A549	25.0	Brain (Amygdala) Pool	12.6
Lung ca. NCI-H526	6.4	Brain (cerebellum)	37.1
Lung ca. NCI-H23	10.2	Brain (fetal)	13.6
Lung ca. NCI-H460	8.7	Brain (Hippocampus) Pool	15.3
Lung ca. HOP-62	11.3	Cerebral Cortex Pool	15.6
Lung ca. NCI-H522	16.8	Brain (Substantia nigra) Pool	27.0
Liver	2.5	Brain (Thalamus) Pool	17.0
Fetal Liver	6.6	Brain (whole)	8.9
Liver ca. HepG2	16.3	Spinal Cord Pool	19.9
Kidney Pool	24.0	Adrenal Gland	9.9
Fetal Kidney	8.0	Pituitary gland Pool	6.3
Renal ca. 786-0	11.4	Salivary Gland	7.2
Renal ca. A498	21.2	Thyroid (female)	12.1
Renal ca. ACHN	10.2	Pancreatic ca. CAPAN2	35.1
Renal ca. UO-31	18.3	Pancreas Pool	23.3

Table DJD. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag3647, Run	Rel. Exp.(%) Ag3647, Run	Tissue Name	Rel. Exp.(%) Ag3647, Run	Rel. Exp.(%) Ag3647, Run
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	169975750	197444046		169975750	197444046
Secondary Th1 act	7.7	7.1	HUVEC IL-1beta	20.4	22.1
Secondary Th2 act	10.7	8.7	HUVEC IFN gamma	21.5	21.6
Secondary Tr1 act	9.1	7.9	HUVEC TNF alpha + IFN gamma	39.2	26.2
Secondary Th1 rest	4.2	2.7	HUVEC TNF alpha + IL4	20.9	16.6
Secondary Th2 rest	6.0	6.2	HUVEC IL-11	8.5	8.8
Secondary Tr1 rest	5.0	4.0	Lung Microvascular EC none	29.9	31.0
Primary Th1 act	8.1	6.3	Lung Microvascular EC TNFalpha + IL- 1beta	37.4	24.1
Primary Th2 act	9.0	9.5	Microvascular Dermal EC none	17.9	12.4
Primary Tr1 act	10.1	10.7	Microvascular Dermal EC TNFalpha + IL- 1beta	20.0	15.6
Primary Th1 rest	6.0	2.3	Bronchial epithelium TNFalpha + IL1beta	41.5	34.6
Primary Th2 rest	4.3	1.1	Small airway epithelium none	37.4	33.2
Primary Tr1 rest	7.4	5.4	Small airway epithelium TNFalpha + IL- 1beta	58.2	43.8
CD45RA CD4 lymphocyte act	4.2	4.2	Coronary artery SMC rest	6.3	8.0
CD45RO CD4 lymphocyte act	7.1	5.7	Coronary artery SMC TNFalpha + IL-1beta	9.7	7.8
CD8 lymphocyte act	6.2	4.5	Astrocytes rest	11.7	4.2
Secondary CD8 lymphocyte rest	9.7	8.5	Astrocytes TNFalpha + IL- 1beta	11.1	7.2
Secondary CD8 lymphocyte act	6.5	3.7	KU-812 (Basophil) rest	10.0	7.9
CD4 lymphocyte none	1.8	1.7	KU-812 (Basophil)	14.4	13.3

			PMA/ionomycin		
2ry Th1/Th2/Tr1_anti- CD95 CH11	3.1	2.9	CCD1106 (Keratinocytes) none	42.0	46.7
LAK cells rest	9.9	5.9	CCD1106 (Keratinocytes) TNFalpha + IL- 1beta	100.0	100.0
LAK cells IL-2	5.3	4.5	Liver cirrhosis	14.7	16.2
LAK cells IL-2+IL- 12	9.2	3.2	NCI-H292 none	17.1	16.2
LAK cells IL- 2+IFN gamma	6.1	3.8	NCI-H292 IL-4	19.1	25.0
LAK cells IL-2+ IL-18	11.3	5.5	NCI-H292 IL-9	25.7	23.8
LAK cells PMA/ionomycin	20.9	16.2	NCI-H292 IL-13	20.6	18.8
NK Cells IL-2 rest	8.2	12.1	NCI-H292 IFN gamma	42.6	28.3
Two Way MLR 3 day	9.2	11.4	HPAEC none	13.6	11.7
Two Way MLR 5 day	8.4	4.9	HPAEC TNF alpha + IL-1 beta	20.3	22.1
Two Way MLR 7 day	8.7	5.8	Lung fibroblast none	16.4	17.3
PBMC rest	3.0	2.2	Lung fibroblast TNF alpha + IL-1 beta	11.6	13.6
PBMC PWM	11.0	7.6	Lung fibroblast IL-4	14.6	28.3
PBMC PHA-L	9.1	4.6	Lung fibroblast IL-9	16.3	23.8
Ramos (B cell) none	5.2	3.6	Lung fibroblast IL-13	14.7	12.9
Ramos (B cell) ionomycin	5.1	4.9	Lung fibroblast IFN gamma	22.7	23.8
B lymphocytes PWM	4.1	3.8	Dermal fibroblast CCD1070 rest	12.0	13.6
B lymphocytes CD40L and IL-4	8.4	4.9	Dermal fibroblast CCD1070 TNF alpha	10.9	14.7
EOL-1 dbcAMP	7.3	5.5	Dermal fibroblast CCD1070 IL-1 beta	10.0	4.4
EOL-1 dbcAMP PMA/ionomycin	8.4	7.8	Dermal fibroblast IFN gamma	9.2	7.7

Dendritic cells none	7.5	8.0	Dermal fibroblast IL-4	9.7	7.5
Dendritic cells LPS	5.7	4.6	Dermal Fibroblasts rest	10.1	8.5
Dendritic cells anti-CD40	7.7	6.9	Neutrophils TNFa+LPS	11.4	5.8
Monocytes rest	8.5	7.5	Neutrophils rest	3.0	3.0
Monocytes LPS	24.8	25.9	Colon	13.0	9.6
Macrophages rest	8.4	5.6	Lung	16.4	8.4
Macrophages LPS	12.2	5.9	Thymus	10.9	8.8
HUVEC none	8.7	12.8	Kidney	6.3	4.7
HUVEC starved	11.8	11.7			

CNS_neurodegeneration_v1.0 Summary: Ag3647 This panel confirms the expression of this gene at moderate levels in the brains of an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. Please see Panel 1.4 for a discussion of the potential utility of this gene in treatment of central nervous system disorders.

General_screening_panel_v1.4 Summary: Ag3647 Expression of the CG88613-01 gene is highest in a gastric cancer cell line (CT = 28). Expression of this gene appears to be upregulated in a number of cancer cell lines when compared to normal tissues. Specifically, CG88613-01 gene expression is somewhat higher in breast and ovarian cancers when compared to their respective normal tissues. Thus, therapeutic modulation of the activity of this gene or its protein product, using small molecule drugs, antibodies or protein therapeutics, may be of benefit in the treatment of gastric, breast and ovarian cancer.

In addition, this gene is expressed at moderate levels in all regions of the central nervous system examined, including amygdala, hippocampus, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord. The CG88613-01 gene encodes a protein that is identical to a protein now known in the public domain as inositol 1,4,5-triphosphate 3-kinase C (ref. 1). Inositol 1,4,5-trisphosphate 3-kinase (ITPK) catalyzes the phosphorylation of Ins(1,4,5)P3 to Ins(1,4,5)P4, both of which are modulators of calcium homeostasis. Calcium is one of the most important intracellular messengers in the brain, being essential for neuronal development, synaptic transmission and plasticity, and the regulation of various metabolic pathways (ref. 2). Therefore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression. Furthermore, this gene is also expressed in tissues with metabolic or endocrine

function, including pancreas, adipose, adrenal gland, thyroid, pituitary gland, skeletal muscle, heart, liver and the gastrointestinal tract. Therefore, therapeutic modulation of the activity of this gene may prove useful in the treatment of endocrine/metabolically related diseases, such as obesity and diabetes.

References:

1. Dewaste V, Pouillon V, Moreau C, Shears S, Takazawa K, Erneux C. Cloning and expression of a cDNA encoding human inositol 1,4,5-trisphosphate 3-kinase C. *Biochem J* 2000 Dec 1;352 Pt 2:343-51

2. Mattson MP, Chan SL. Dysregulation of cellular calcium homeostasis in Alzheimer's disease: bad genes and bad habits. *J Mol Neurosci* 2001 Oct;17(2):205-24

Panel 4.1D Summary: Ag3647 Results from two experiments using the same probe/primer set are in excellent agreement. Expression of the CG88613-01 gene is highest in keratinocytes treated with the inflammatory cytokines TNF- α and IL-1 β (CT = 29.5). Therefore, modulation of the expression or activity of this protein through the application of small molecule therapeutics may be useful in the treatment of psoriasis and wound healing.

This gene is also expressed at moderate levels in small airway epithelial cells, bronchial epithelium, and lung microvascular endothelial cells. Endothelial cells are known to play important roles in inflammatory responses by altering the expression of surface proteins that are involved in activation and recruitment of effector inflammatory cells (ref. 1). Expression in small airway epithelial cells, bronchial epithelium, lung microvascular endothelial cells suggests that the protein encoded by this transcript may be involved in lung disorders including asthma, allergies, chronic obstructive pulmonary disease, and emphysema. This gene is homologous to PI-3-kinase which is involved in cell survival and receptor signaling of a number of cells of importance in the immune response in health and disease, including lung pathologies. Therefore, Small molecule antagonists of this gene product may lead to amelioration of symptoms associated with asthma, allergies, chronic obstructive pulmonary disease, and emphysema.

This gene is expressed at low levels in the remainder of the samples on this panel, suggesting that the gene product may play an important role in homeostasis of a number of cell types.

References:

1. Siddiqui RA, English D. Phosphatidylinositol 3'-kinase-mediated calcium mobilization regulates chemotaxis in phosphatidic acid-stimulated human neutrophils. *Biochim Biophys Acta* 2000 Jan 3;1483(1):161-73
2. Condliffe AM, Cadwallader KA, Walker TR, Rintoul RC, Cowburn AS, Chilvers ER. Phosphoinositide 3-kinase: a critical signalling event in pulmonary cells. *Respir Res* 2000;1(1):24-9

DK. CG59993-01 and CG59993-02: synaptotagmin II

Expression of gene CG59993-01 and variant CG59993-02 was assessed using the primer-probe set Ag3645, described in Table DKA. Results of the RTQ-PCR runs are shown in Tables DKB, DKC and DKD.

Table DKA. Probe Name Ag3645

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5' -gaagaagaccctgaaccatac-3'	22	1056	746
Probe	TET-5' -agctttgagatccccctcgagcagat-3' - TAMRA	26	1093	747
Reverse	5' -tgaccactacctggactttctg-3'	22	1120	748

Table DKB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3645, Run 211019104	Tissue Name	Rel. Exp.(%) Ag3645, Run 211019104
AD 1 Hippo	0.4	Control (Path) 3 Temporal Ctx	0.2
AD 2 Hippo	0.2	Control (Path) 4 Temporal Ctx	7.2
AD 3 Hippo	0.0	AD 1 Occipital Ctx	8.7
AD 4 Hippo	0.1	AD 2 Occipital Ctx (Missing)	0.0
AD 5 hippo	100.0	AD 3 Occipital Ctx	0.6
AD 6 Hippo	1.5	AD 4 Occipital Ctx	10.7
Control 2 Hippo	0.9	AD 5 Occipital Ctx	19.2
Control 4 Hippo	0.1	AD 6 Occipital Ctx	57.8
Control (Path) 3 Hippo	0.0	Control 1 Occipital Ctx	0.3

AD 1 Temporal Ctx	0.8	Control 2 Occipital Ctx	81.8
AD 2 Temporal Ctx	2.8	Control 3 Occipital Ctx	11.0
AD 3 Temporal Ctx	0.3	Control 4 Occipital Ctx	0.5
AD 4 Temporal Ctx	2.6	Control (Path) 1 Occipital Ctx	29.1
AD 5 Inf Temporal Ctx	50.0	Control (Path) 2 Occipital Ctx	8.5
AD 5 Sup Temporal Ctx	0.9	Control (Path) 3 Occipital Ctx	0.7
AD 6 Inf Temporal Ctx	2.8	Control (Path) 4 Occipital Ctx	12.8
AD 6 Sup Temporal Ctx	8.2	Control 1 Parietal Ctx	0.4
Control 1 Temporal Ctx	0.1	Control 2 Parietal Ctx	2.3
Control 2 Temporal Ctx	7.2	Control 3 Parietal Ctx	28.7
Control 3 Temporal Ctx	1.5	Control (Path) 1 Parietal Ctx	33.2
Control 4 Temporal Ctx	0.7	Control (Path) 2 Parietal Ctx	21.8
Control (Path) 1 Temporal Ctx	4.7	Control (Path) 3 Parietal Ctx	0.5
Control (Path) 2 Temporal Ctx	6.8	Control (Path) 4 Parietal Ctx	68.3

Table DKC. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3645, Run 218341901	Tissue Name	Rel. Exp.(%) Ag3645, Run 218341901
Adipose	0.0	Renal ca. TK-10	0.1
Melanoma* Hs688(A).T	0.1	Bladder	0.1
Melanoma* Hs688(B).T	0.1	Gastric ca. (liver met.) NCI-N87	0.0
Melanoma* M14	0.0	Gastric ca. KATO III	0.0
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.0
Melanoma* SK-MEL-5	0.4	Colon ca. SW480	0.0
Squamous cell carcinoma SCC-4	0.1	Colon ca.* (SW480 met) SW620	0.0

Testis Pool	1.0	Colon ca. HT29	0.0
Prostate ca.* (bone met) PC-3	0.0	Colon ca. HCT-116	0.0
Prostate Pool	0.1	Colon ca. CaCo-2	0.6
Placenta	0.0	Colon cancer tissue	0.0
Uterus Pool	0.0	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	0.2	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV-3	0.0	Colon ca. SW-48	0.2
Ovarian ca. OVCAR-4	0.2	Colon Pool	0.2
Ovarian ca. OVCAR-5	0.1	Small Intestine Pool	0.1
Ovarian ca. IGROV-1	0.0	Stomach Pool	0.1
Ovarian ca. OVCAR-8	0.0	Bone Marrow Pool	0.0
Ovary	0.7	Fetal Heart	0.1
Breast ca. MCF-7	0.0	Heart Pool	0.0
Breast ca. MDA-MB-231	1.4	Lymph Node Pool	1.0
Breast ca. BT 549	0.2	Fetal Skeletal Muscle	0.0
Breast ca. T47D	0.1	Skeletal Muscle Pool	0.0
Breast ca. MDA-N	0.0	Spleen Pool	0.1
Breast Pool	0.2	Thymus Pool	0.5
Trachea	0.2	CNS cancer (glio/astro) U87-MG	0.0
Lung	0.3	CNS cancer (glio/astro) U-118-MG	0.0
Fetal Lung	0.5	CNS cancer (neuro;met) SK-N-AS	0.2
Lung ca. NCI-N417	0.5	CNS cancer (astro) SF-539	0.0
Lung ca. LX-1	0.0	CNS cancer (astro) SNB-75	0.2
Lung ca. NCI-H146	0.1	CNS cancer (glio) SNB-19	0.0
Lung ca. SHP-77	0.3	CNS cancer (glio) SF-295	0.1
Lung ca. A549	0.0	Brain (Amygdala) Pool	5.9
Lung ca. NCI-H526	0.0	Brain (cerebellum)	100.0
Lung ca. NCI-H23	0.2	Brain (fetal)	0.9
Lung ca. NCI-H460	0.0	Brain (Hippocampus)	2.1

		Pool	
Lung ca. HOP-62	0.0	Cerebral Cortex Pool	19.3
Lung ca. NCI-H522	0.0	Brain (Substantia nigra) Pool	19.5
Liver	0.0	Brain (Thalamus) Pool	14.1
Fetal Liver	0.0	Brain (whole)	10.0
Liver ca. HepG2	0.0	Spinal Cord Pool	15.9
Kidney Pool	0.1	Adrenal Gland	0.9
Fetal Kidney	0.6	Pituitary gland Pool	0.0
Renal ca. 786-0	0.0	Salivary Gland	0.0
Renal ca. A498	0.0	Thyroid (female)	0.1
Renal ca. ACHN	0.0	Pancreatic ca. CAPAN2	0.0
Renal ca. UO-31	0.0	Pancreas Pool	0.8

Table DKD. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag3645, Run 169975206	Tissue Name	Rel. Exp.(%) Ag3645, Run 169975206
Secondary Th1 act	0.0	HUVEC IL-1beta	0.0
Secondary Th2 act	0.0	HUVEC IFN gamma	0.0
Secondary Tr1 act	0.0	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	0.0	HUVEC IL-11	0.0
Secondary Tr1 rest	0.0	Lung Microvascular EC none	0.0
Primary Th1 act	0.0	Lung Microvascular EC TNFalpha + IL-1beta	0.0
Primary Th2 act	0.0	Microvascular Dermal EC none	0.0
Primary Tr1 act	0.0	Microvascular Dermal EC TNFalpha + IL-1beta	0.0
Primary Th1 rest	0.0	Bronchial epithelium TNFalpha + IL1beta	0.0
Primary Th2 rest	0.0	Small airway epithelium none	0.0
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	0.0
CD45RA CD4 lymphocyte act	0.0	Coronary artery SMC rest	0.0
CD45RO CD4 lymphocyte act	0.0	Coronary artery SMC TNFalpha + IL-1beta	0.0
CD8 lymphocyte act	0.0	Astrocytes rest	0.0

Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFalpha + IL-1beta	100.0
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	0.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.0	CCD1106 (Keratinocytes) none	0.0
LAK cells rest	0.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0
LAK cells IL-2	0.0	Liver cirrhosis	0.0
LAK cells IL-2+IL-12	0.0	NCI-H292 none	15.0
LAK cells IL-2+IFN gamma	8.3	NCI-H292 IL-4	0.0
LAK cells IL-2+ IL-18	0.0	NCI-H292 IL-9	22.5
LAK cells PMA/ionomycin	0.0	NCI-H292 IL-13	0.0
NK Cells IL-2 rest	0.0	NCI-H292 IFN gamma	0.0
Two Way MLR 3 day	0.0	HPAEC none	0.0
Two Way MLR 5 day	0.0	HPAEC TNF alpha + IL-1 beta	0.0
Two Way MLR 7 day	0.0	Lung fibroblast none	0.0
PBMC rest	0.0	Lung fibroblast TNF alpha + IL-1 beta	4.3
PBMC PWM	0.0	Lung fibroblast IL-4	0.0
PBMC PHA-L	12.9	Lung fibroblast IL-9	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-13	36.9
Ramos (B cell) ionomycin	0.0	Lung fibroblast IFN gamma	0.0
B lymphocytes PWM	0.0	Dermal fibroblast CCD1070 rest	0.0
B lymphocytes CD40L and IL-4	0.0	Dermal fibroblast CCD1070 TNF alpha	0.0
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 IL-1 beta	0.0
EOL-1 dbcAMP PMA/ionomycin	48.6	Dermal fibroblast IFN gamma	0.0
Dendritic cells none	0.0	Dermal fibroblast IL-4	0.0
Dendritic cells LPS	0.0	Dermal Fibroblasts rest	0.0
Dendritic cells anti-CD40	20.9	Neutrophils TNFa+LPS	0.0
Monocytes rest	0.0	Neutrophils rest	0.0
Monocytes LPS	0.0	Colon	25.7
Macrophages rest	0.0	Lung	28.7

Macrophages LPS	0.0	Thymus	43.2
HUVEC none	0.0	Kidney	25.9
HUVEC starved	0.0		

CNS_neurodegeneration_v1.0 Summary: Ag3645 While no association between the expression of the CG59993-01 gene and the presence of Alzheimer's disease is detected in this panel, these results confirm the expression of this gene in areas that degenerate in Alzheimer's disease, including the cortex and hippocampus. Synaptotagmin expression is altered in the brain of Alzheimer's patients, possibly explaining impaired synaptogenesis and/or synaptosomal loss secondary to neuronal loss observed in the neurodegenerative disorder. It may also represent, reflect or account for the impaired neuronal transmission in Alzheimer's disease (AD), caused by deterioration of the exocytic machinery. Since the this gene is a homolog of synaptotagmin, agents that potentiate the expression or function of the protein encoded by the this gene may be useful in the treatment of Alzheimer's disease.

General_screening_panel_v1.4 Summary: Ag3645 The CG59993-01 gene is a homolog of synaptotagmin, and shows high to moderate expression across all brain regions with highest expression in the cerebellum (CT = 26.4) Synaptotagmin is a presynaptic protein involved in synaptic vesicle release, making this an ideal drug target for diseases such as epilepsy, in which reduction of neurotransmission is beneficial. Selective inhibition of this gene or its protein product may therefore be useful in the treatment of seizure disorders. Furthermore, selective inhibition of neural transmission through antagonism of the protein encoded by this gene may show therapeutic benefit in psychiatric diseases where it is believed that inappropriate neural connections have been established, such as schizophrenia and bipolar disorder. In addition, antibodies against synaptotagmin may cause Lambert-Eaton myasthenic syndrome. Therefore, peptide fragments of the protein encoded by this gene may serve to block the action of these antibodies and treat Lambert-Eaton myasthenic syndrome.

Panel 4.1D Summary: Ag3645 Expression of the CG59993-01 gene is restricted to a sample derived from astrocytes treated with TNF-alpha and IL-1 beta (CT=33.9). This expression in samples related to the central nervous system is consistent with results of the previous panels and suggests that modulation of this protein could be beneficial in the treatment of CNS disease-associated inflammation or neurodegeneration, including multiple sclerosis.

DL. CG59991-01: OOPASM SPECIFIC PROTEIN

Expression of gene CG59991-01 was assessed using the primer-probe set Ag3644, described in Table DLA. Results of the RTQ-PCR runs are shown in Tables DLB and DLC.

Table DLA. Probe Name Ag3644

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-gggagtaatgcctctcagtga-3'	21	2294	749
Probe	TET-5'-cttgagagtctcccagtgcgccct-3'- TAMRA	24	2318	750
Reverse	5'-atgccacagtcctccagtatc-3'	21	2351	751

Table DLB. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3644, Run 218306573	Tissue Name	Rel. Exp.(%) Ag3644, Run 218306573
Adipose	0.0	Renal ca. TK-10	0.0
Melanoma* Hs688(A).T	0.0	Bladder	0.0
Melanoma* Hs688(B).T	0.0	Gastric ca. (liver met.) NCI-N87	0.0
Melanoma* M14	0.0	Gastric ca. KATO III	0.1
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.0
Melanoma* SK- MEL-5	0.0	Colon ca. SW480	0.0
Squamous cell carcinoma SCC-4	0.0	Colon ca.* (SW480 met) SW620	0.0
Testis Pool	0.5	Colon ca. HT29	0.0
Prostate ca.* (bone met) PC-3	0.0	Colon ca. HCT-116	0.1
Prostate Pool	0.0	Colon ca. CaCo-2	0.0
Placenta	0.0	Colon cancer tissue	0.0
Uterus Pool	0.0	Colon ca. SW1116	0.0
Ovarian ca. OVCAR 3	0.0	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV- 3	0.0	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	0.6	Colon Pool	0.0
Ovarian ca. OVCAR-5	0.0	Small Intestine Pool	0.0
Ovarian ca. IGROV- 1	0.0	Stomach Pool	0.0

Ovarian ca. OVCAR-8	0.0	Bone Marrow Pool	0.0
Ovary	0.0	Fetal Heart	0.0
Breast ca. MCF-7	0.0	Heart Pool	0.0
Breast ca. MDA-MB-231	0.0	Lymph Node Pool	0.0
Breast ca. BT 549	0.0	Fetal Skeletal Muscle	0.0
Breast ca. T47D	0.0	Skeletal Muscle Pool	0.0
Breast ca. MDA-N	0.0	Spleen Pool	0.0
Breast Pool	0.0	Thymus Pool	0.0
Trachea	0.0	CNS cancer (glio/astro) U87-MG	0.0
Lung	0.0	CNS cancer (glio/astro) U-118-MG	0.0
Fetal Lung	0.0	CNS cancer (neuro;met) SK-N-AS	0.0
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF-539	0.0
Lung ca. LX-1	0.0	CNS cancer (astro) SNB-75	0.0
Lung ca. NCI-H146	0.0	CNS cancer (glio) SNB-19	0.0
Lung ca. SHP-77	100.0	CNS cancer (glio) SF-295	0.3
Lung ca. A549	0.0	Brain (Amygdala) Pool	0.0
Lung ca. NCI-H526	0.0	Brain (cerebellum)	0.0
Lung ca. NCI-H23	0.0	Brain (fetal)	0.0
Lung ca. NCI-H460	0.0	Brain (Hippocampus) Pool	0.0
Lung ca. HOP-62	0.0	Cerebral Cortex Pool	0.0
Lung ca. NCI-H522	0.0	Brain (Substantia nigra) Pool	0.0
Liver	0.0	Brain (Thalamus) Pool	0.0
Fetal Liver	0.0	Brain (whole)	0.0
Liver ca. HepG2	0.0	Spinal Cord Pool	0.0
Kidney Pool	0.0	Adrenal Gland	0.0
Fetal Kidney	0.0	Pituitary gland Pool	0.0
Renal ca. 786-0	0.0	Salivary Gland	0.0
Renal ca. A498	0.0	Thyroid (female)	0.1
Renal ca. ACHN	0.0	Pancreatic ca. CAPAN2	0.0
Renal ca. UO-31	0.0	Pancreas Pool	0.1

Table DLC. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag3644, Run 169975188	Tissue Name	Rel. Exp.(%) Ag3644, Run 169975188
Secondary Th1 act	0.0	HUVEC IL-1beta	0.0
Secondary Th2 act	0.0	HUVEC IFN gamma	0.0
Secondary Tr1 act	0.0	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	0.0	HUVEC IL-11	0.0
Secondary Tr1 rest	0.0	Lung Microvascular EC none	0.0
Primary Th1 act	0.0	Lung Microvascular EC TNFalpha + IL-1beta	0.0
Primary Th2 act	0.0	Microvascular Dermal EC none	0.0
Primary Tr1 act	0.0	Microvascular Dermal EC TNFalpha + IL-1beta	0.0
Primary Th1 rest	0.0	Bronchial epithelium TNFalpha + IL1beta	0.0
Primary Th2 rest	0.0	Small airway epithelium none	0.0
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	0.0
CD45RA CD4 lymphocyte act	0.0	Coronary artery SMC rest	0.0
CD45RO CD4 lymphocyte act	0.0	Coronary artery SMC TNFalpha + IL-1beta	0.0
CD8 lymphocyte act	0.0	Astrocytes rest	0.0
Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFalpha + IL-1beta	0.0
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	48.3
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	100.0
2ry Th1/Th2/Tr1_anti- CD95 CH11	0.0	CCD1106 (Keratinocytes) none	0.0
LAK cells rest	0.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0
LAK cells IL-2	0.0	Liver cirrhosis	0.0
LAK cells IL-2+IL-12	0.0	NCI-H292 none	0.0
LAK cells IL-2+IFN gamma	0.0	NCI-H292 IL-4	0.0
LAK cells IL-2+ IL-18	0.0	NCI-H292 IL-9	0.0
LAK cells PMA/ionomycin	0.0	NCI-H292 IL-13	0.0

NK Cells IL-2 rest	0.0	NCI-H292 IFN gamma	0.0
Two Way MLR 3 day	0.0	HPAEC none	0.0
Two Way MLR 5 day	0.0	HPAEC TNF alpha + IL-1 beta	0.0
Two Way MLR 7 day	0.0	Lung fibroblast none	0.0
PBMC rest	0.0	Lung fibroblast TNF alpha + IL-1 beta	0.0
PBMC PWM	0.0	Lung fibroblast IL-4	0.0
PBMC PHA-L	0.0	Lung fibroblast IL-9	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-13	0.0
Ramos (B cell) ionomycin	0.0	Lung fibroblast IFN gamma	0.0
B lymphocytes PWM	0.0	Dermal fibroblast CCD1070 rest	0.0
B lymphocytes CD40L and IL-4	0.0	Dermal fibroblast CCD1070 TNF alpha	0.0
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 IL-1 beta	0.0
EOL-1 dbcAMP PMA/ionomycin	0.0	Dermal fibroblast IFN gamma	0.0
Dendritic cells none	0.0	Dermal fibroblast IL-4	0.0
Dendritic cells LPS	0.0	Dermal Fibroblasts rest	0.0
Dendritic cells anti-CD40	0.0	Neutrophils TNFa+LPS	0.0
Monocytes rest	0.0	Neutrophils rest	0.0
Monocytes LPS	0.0	Colon	0.0
Macrophages rest	0.0	Lung	0.0
Macrophages LPS	0.0	Thymus	0.0
HUVEC none	0.0	Kidney	0.0
HUVEC starved	0.0		

CNS_neurodegeneration_v1.0 Summary: Ag3644 Expression of the CG59991-01 gene is low/undetectable in all samples on this panel (CTs>35). (Data not shown).

General_screening_panel_v1.4 Summary: Ag3644 Expression of the CG59991-01 gene is restricted to a sample derived from a lung cancer cell line (CT=27.2). Thus, expression of this gene could be used to differentiate between this sample and other samples on this panel and as a marker to detect the presence of lung cancer. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of lung cancer.

Panel 4.1D Summary: Ag3644 Expression of the CG59991-01 gene is restricted to samples derived from the basophil cell line KU-812 (CTs=32). Thus, expression of this gene could be

used as a marker of this cell type. Basophils release histamines and other biological modifiers in repose to allergens and play an important role in the pathology of asthma and hypersensitivity reactions. Therefore, the specific pattern of expression of this gene suggests that therapeutic modulation of the expression or function of the protein encoded by this gene may block or inhibit inflammation or tissue damage due to basophil activation in response to asthma, allergies, hypersensitivity reactions, psoriasis, and viral infections.

DM. CG59987-01 and CG59987-02: RHOPHILIN

Expression of gene CG59987-01 and full length clone CG59987-02 was assessed using the primer-probe set Ag3643, described in Table DMA. Results of the RTQ-PCR runs are shown in Tables DMB and DMC. Please note that CG59987-02 represents a full-length physical clone of the CG59987-01 gene, validating the prediction of the gene sequence.

Table DMA. Probe Name Ag3643

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-tacttttcggaagggtgtaatc-3'	22	103	752
Probe	TET-5'-cttgcacaaaccggccggagtaaatt-3'- TAMRA	26	127	753
Reverse	5'-tgattcaaagcagctctttgat-3'	22	158	754

Table DMB. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3643, Run 218306426	Tissue Name	Rel. Exp.(%) Ag3643, Run 218306426
Adipose	1.4	Renal ca. TK-10	17.2
Melanoma* Hs688(A).T	0.5	Bladder	9.1
Melanoma* Hs688(B).T	0.6	Gastric ca. (liver met.) NCI-N87	46.7
Melanoma* M14	6.3	Gastric ca. KATO III	39.2
Melanoma* LOXIMVI	1.7	Colon ca. SW-948	16.6
Melanoma* SK- MEL-5	8.7	Colon ca. SW480	7.0
Squamous cell carcinoma SCC-4	5.4	Colon ca.* (SW480 met) SW620	0.4
Testis Pool	0.5	Colon ca. HT29	24.8
Prostate ca.* (bone met) PC-3	7.7	Colon ca. HCT-116	26.8

Prostate Pool	6.6	Colon ca. CaCo-2	34.2
Placenta	3.3	Colon cancer tissue	13.0
Uterus Pool	0.4	Colon ca. SW1116	4.5
Ovarian ca. OVCAR-3	44.1	Colon ca. Colo-205	5.5
Ovarian ca. SK-OV-3	36.9	Colon ca. SW-48	6.5
Ovarian ca. OVCAR-4	58.6	Colon Pool	0.9
Ovarian ca. OVCAR-5	50.7	Small Intestine Pool	1.9
Ovarian ca. IGROV-1	20.3	Stomach Pool	2.3
Ovarian ca. OVCAR-8	7.9	Bone Marrow Pool	0.3
Ovary	1.6	Fetal Heart	0.7
Breast ca. MCF-7	17.4	Heart Pool	0.4
Breast ca. MDA-MB-231	13.7	Lymph Node Pool	1.0
Breast ca. BT 549	8.2	Fetal Skeletal Muscle	0.1
Breast ca. T47D	100.0	Skeletal Muscle Pool	0.2
Breast ca. MDA-N	4.7	Spleen Pool	0.2
Breast Pool	1.9	Thymus Pool	1.5
Trachea	8.4	CNS cancer (glio/astro) U87-MG	1.0
Lung	0.3	CNS cancer (glio/astro) U-118-MG	1.3
Fetal Lung	6.9	CNS cancer (neuro;met) SK-N-AS	5.2
Lung ca. NCI-N417	0.9	CNS cancer (astro) SF-539	2.5
Lung ca. LX-1	0.2	CNS cancer (astro) SNB-75	6.0
Lung ca. NCI-H146	1.9	CNS cancer (glio) SNB-19	21.6
Lung ca. SHP-77	0.0	CNS cancer (glio) SF-295	14.7
Lung ca. A549	54.3	Brain (Amygdala) Pool	1.0
Lung ca. NCI-H526	3.7	Brain (cerebellum)	5.2
Lung ca. NCI-H23	3.2	Brain (fetal)	0.7
Lung ca. NCI-H460	1.2	Brain (Hippocampus) Pool	1.9
Lung ca. HOP-62	6.5	Cerebral Cortex Pool	2.3
Lung ca. NCI-H522	3.7	Brain (Substantia nigra)	2.1

		Pool	
Liver	1.5	Brain (Thalamus) Pool	2.7
Fetal Liver	5.6	Brain (whole)	3.5
Liver ca. HepG2	7.0	Spinal Cord Pool	3.6
Kidney Pool	1.4	Adrenal Gland	0.2
Fetal Kidney	3.4	Pituitary gland Pool	1.3
Renal ca. 786-0	12.2	Salivary Gland	6.7
Renal ca. A498	8.8	Thyroid (female)	1.2
Renal ca. ACHN	9.1	Pancreatic ca. CAPAN2	21.3
Renal ca. UO-31	9.9	Pancreas Pool	12.2

Table DMC. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag3643, Run 169975145	Tissue Name	Rel. Exp.(%) Ag3643, Run 169975145
Secondary Th1 act	3.8	HUVEC IL-1beta	6.9
Secondary Th2 act	1.1	HUVEC IFN gamma	4.4
Secondary Tr1 act	0.9	HUVEC TNF alpha + IFN gamma	2.6
Secondary Th1 rest	0.5	HUVEC TNF alpha + IL4	4.0
Secondary Th2 rest	0.9	HUVEC IL-11	2.5
Secondary Tr1 rest	0.6	Lung Microvascular EC none	4.3
Primary Th1 act	1.8	Lung Microvascular EC TNFalpha + IL-1beta	1.5
Primary Th2 act	5.0	Microvascular Dermal EC none	6.7
Primary Tr1 act	3.4	Microvascular Dermal EC TNFalpha + IL-1beta	7.7
Primary Th1 rest	1.0	Bronchial epithelium TNFalpha + IL1beta	17.7
Primary Th2 rest	0.8	Small airway epithelium none	13.7
Primary Tr1 rest	0.9	Small airway epithelium TNFalpha + IL-1beta	23.3
CD45RA CD4 lymphocyte act	3.5	Coronary artery SMC rest	6.7
CD45RO CD4 lymphocyte act	3.0	Coronary artery SMC TNFalpha + IL-1beta	4.3
CD8 lymphocyte act	6.2	Astrocytes rest	35.4
Secondary CD8 lymphocyte rest	3.4	Astrocytes TNFalpha + IL-1beta	24.3
Secondary CD8	0.0	KU-812 (Basophil) rest	0.5

lymphocyte act			
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	2.3
2ry Th1/Th2/Tr1_anti- CD95 CH11	0.0	CCD1106 (Keratinocytes) none	39.8
LAK cells rest	0.7	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	32.5
LAK cells IL-2	0.4	Liver cirrhosis	41.2
LAK cells IL-2+IL-12	1.3	NCI-H292 none	49.3
LAK cells IL-2+IFN gamma	2.2	NCI-H292 IL-4	45.1
LAK cells IL-2+ IL-18	2.0	NCI-H292 IL-9	100.0
LAK cells PMA/ionomycin	1.7	NCI-H292 IL-13	51.8
NK Cells IL-2 rest	0.5	NCI-H292 IFN gamma	53.6
Two Way MLR 3 day	0.4	HPAEC none	8.0
Two Way MLR 5 day	0.8	HPAEC TNF alpha + IL-1 beta	6.1
Two Way MLR 7 day	1.5	Lung fibroblast none	13.3
PBMC rest	0.6	Lung fibroblast TNF alpha + IL-1 beta	7.1
PBMC PWM	4.3	Lung fibroblast IL-4	3.6
PBMC PHA-L	3.6	Lung fibroblast IL-9	8.5
Ramos (B cell) none	14.8	Lung fibroblast IL-13	3.3
Ramos (B cell) ionomycin	15.7	Lung fibroblast IFN gamma	10.5
B lymphocytes PWM	6.3	Dermal fibroblast CCD1070 rest	5.1
B lymphocytes CD40L and IL-4	6.5	Dermal fibroblast CCD1070 TNF alpha	5.6
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 IL-1 beta	7.7
EOL-1 dbcAMP PMA/ionomycin	0.0	Dermal fibroblast IFN gamma	5.5
Dendritic cells none	0.5	Dermal fibroblast IL-4	3.7
Dendritic cells LPS	0.0	Dermal Fibroblasts rest	1.5
Dendritic cells anti- CD40	0.0	Neutrophils TNFa+LPS	0.0
Monocytes rest	0.0	Neutrophils rest	0.0
Monocytes LPS	0.3	Colon	34.6
Macrophages rest	0.4	Lung	4.3
Macrophages LPS	0.0	Thymus	9.9
HUVEC none	3.3	Kidney	51.4
HUVEC starved	3.4		

CNS_neurodegeneration_v1.0 Summary: Ag3643 Results from one experiment with the CG59987-01 gene are not included. The amp plot indicates that there were experimental difficulties with this run.

General_screening_panel_v1.4 Summary: Ag3643 Expression of the CG59987-01 gene is highest in a breast cancer cell line (CT=25.3). In addition, significant levels of expression are seen in clusters of cell lines derived from brain, gastric, colon, lung, and ovarian cancers. In addition, expression overall appears to be higher in samples derived from cancer cell lines than in normal tissues. Thus, expression of this gene could be used as a marker to detect the presence of cancer. This gene encodes a homolog of rhophilin, a rho GTPase that is involved in a signaling pathway that regulates cell adhesion, among other functions. Therefore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of these cancers.

Among tissues with metabolic function, this gene is expressed at moderate to low levels in pituitary, adipose, adrenal gland, pancreas, thyroid, skeletal muscle, and adult and fetal heart, and liver. This widespread expression among these tissues suggests that this gene product may play a role in normal neuroendocrine and metabolic and that dysregulated expression of this gene may contribute to neuroendocrine disorders or metabolic diseases, such as obesity and diabetes.

This gene is also expressed at moderate to low levels in the CNS and may be a small molecule target for the treatment of neurologic diseases.

Panel 4.1D Summary: Ag3643 Expression of the CG59987-01 gene is highest in NCI-H292 cells stimulated by IL-9(CT=29.2). The gene is also expressed in a cluster of treated and untreated NCI-H292 mucoidermoid cell line samples. The transcript is also expressed at lower but still significant levels in both small airway and bronchial epithelium treated with IL-1 beta and TNF-alpha. In comparison, expression in the normal lung is relatively low. The expression of the transcript in activated normal epithelium as well as a cell line that is often used as a model for airway epithelium (NCI-H292 cells) suggests that this transcript may be important in the proliferation or activation of airway epithelium. Therefore, therapeutics designed with the protein encoded by this transcript could be important in the treatment of diseases which include lung airway inflammation such as asthma and COPD.

DN. CG59971-01 and CG59971-02: Leucine Rich Repeat protein

Expression of gene CG59971-01 and variant CG59971-02 was assessed using the primer-probe set Ag3639, described in Table DNA. Results of the RTQ-PCR runs are shown in Tables DNB and DNC.

Table DNA. Probe Name Ag3639

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-ttctgccaaacttcagctacaat-3'	22	510	755
Probe	TET-5'-cttagacagctccctgcgcctcttgt-3'- TAMRA	26	543	756
Reverse	5'-acttgattgtggcttaggttca-3'	22	584	757

Table DNB. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3639, Run 218234144	Tissue Name	Rel. Exp.(%) Ag3639, Run 218234144
Adipose	3.2	Renal ca. TK-10	24.0
Melanoma* Hs688(A).T	17.9	Bladder	11.8
Melanoma* Hs688(B).T	12.6	Gastric ca. (liver met.) NCI-N87	35.6
Melanoma* M14	64.6	Gastric ca. KATO III	35.8
Melanoma* LOXIMVI	15.5	Colon ca. SW-948	8.0
Melanoma* SK- MEL-5	25.2	Colon ca. SW480	55.5
Squamous cell carcinoma SCC-4	10.5	Colon ca.* (SW480 met) SW620	32.8
Testis Pool	8.9	Colon ca. HT29	13.7
Prostate ca.* (bone met) PC-3	19.3	Colon ca. HCT-116	34.9
Prostate Pool	3.2	Colon ca. CaCo-2	15.4
Placenta	16.3	Colon cancer tissue	14.3
Uterus Pool	1.0	Colon ca. SW1116	7.9
Ovarian ca. OVCAR-3	19.9	Colon ca. Colo-205	13.3
Ovarian ca. SK-OV- 3	30.1	Colon ca. SW-48	8.8
Ovarian ca. OVCAR-4	14.8	Colon Pool	8.2
Ovarian ca. OVCAR-5	60.7	Small Intestine Pool	7.7
Ovarian ca. IGROV-	15.1	Stomach Pool	3.9

1			
Ovarian ca. OVCAR-8	9.5	Bone Marrow Pool	2.7
Ovary	12.6	Fetal Heart	7.2
Breast ca. MCF-7	54.0	Heart Pool	3.7
Breast ca. MDA-MB-231	31.2	Lymph Node Pool	10.4
Breast ca. BT 549	27.2	Fetal Skeletal Muscle	4.0
Breast ca. T47D	100.0	Skeletal Muscle Pool	3.6
Breast ca. MDA-N	20.4	Spleen Pool	8.4
Breast Pool	8.9	Thymus Pool	15.3
Trachea	10.3	CNS cancer (glio/astro) U87-MG	37.9
Lung	1.1	CNS cancer (glio/astro) U-118-MG	26.2
Fetal Lung	21.9	CNS cancer (neuro;met) SK-N-AS	22.4
Lung ca. NCI-N417	4.5	CNS cancer (astro) SF-539	15.7
Lung ca. LX-1	32.8	CNS cancer (astro) SNB-75	46.7
Lung ca. NCI-H146	7.7	CNS cancer (glio) SNB-19	12.2
Lung ca. SHP-77	33.2	CNS cancer (glio) SF-295	31.4
Lung ca. A549	30.8	Brain (Amygdala) Pool	7.9
Lung ca. NCI-H526	8.7	Brain (cerebellum)	27.4
Lung ca. NCI-H23	23.2	Brain (fetal)	24.3
Lung ca. NCI-H460	18.0	Brain (Hippocampus) Pool	6.8
Lung ca. HOP-62	9.2	Cerebral Cortex Pool	8.0
Lung ca. NCI-H522	22.5	Brain (Substantia nigra) Pool	8.3
Liver	0.8	Brain (Thalamus) Pool	10.7
Fetal Liver	8.8	Brain (whole)	13.8
Liver ca. HepG2	19.3	Spinal Cord Pool	7.6
Kidney Pool	12.9	Adrenal Gland	14.1
Fetal Kidney	8.4	Pituitary gland Pool	6.6
Renal ca. 786-0	20.0	Salivary Gland	3.0
Renal ca. A498	5.2	Thyroid (female)	4.9
Renal ca. ACHN	34.4	Pancreatic ca. CAPAN2	20.9
Renal ca. UO-31	15.5	Pancreas Pool	10.7

Table DNC. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag3639, Run 169975065	Tissue Name	Rel. Exp.(%) Ag3639, Run 169975065
Secondary Th1 act	51.8	HUVEC IL-1beta	27.0
Secondary Th2 act	68.8	HUVEC IFN gamma	31.2
Secondary Tr1 act	74.7	HUVEC TNF alpha + IFN gamma	28.9
Secondary Th1 rest	26.4	HUVEC TNF alpha + IL4	26.4
Secondary Th2 rest	41.5	HUVEC IL-11	22.4
Secondary Tr1 rest	24.1	Lung Microvascular EC none	55.5
Primary Th1 act	50.3	Lung Microvascular EC TNFalpha + IL-1beta	36.1
Primary Th2 act	75.8	Microvascular Dermal EC none	23.5
Primary Tr1 act	66.4	Microvascular Dermal EC TNFalpha + IL-1beta	33.0
Primary Th1 rest	19.8	Bronchial epithelium TNFalpha + IL1beta	22.8
Primary Th2 rest	33.9	Small airway epithelium none	23.2
Primary Tr1 rest	64.2	Small airway epithelium TNFalpha + IL-1beta	37.1
CD45RA CD4 lymphocyte act	35.4	Coronary artery SMC rest	21.2
CD45RO CD4 lymphocyte act	59.5	Coronary artery SMC TNFalpha + IL-1beta	13.4
CD8 lymphocyte act	64.6	Astrocytes rest	23.3
Secondary CD8 lymphocyte rest	36.1	Astrocytes TNFalpha + IL-1beta	25.2
Secondary CD8 lymphocyte act	45.1	KU-812 (Basophil) rest	22.4
CD4 lymphocyte none	20.0	KU-812 (Basophil) PMA/ionomycin	32.8
2ry Th1/Th2/Tr1_anti- CD95 CH11	44.1	CCD1106 (Keratinocytes) none	61.6
LAK cells rest	53.2	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	49.0
LAK cells IL-2	57.4	Liver cirrhosis	8.1
LAK cells IL-2+IL-12	54.0	NCI-H292 none	46.7
LAK cells IL-2+IFN gamma	59.0	NCI-H292 IL-4	45.1
LAK cells IL-2+ IL-18	61.6	NCI-H292 IL-9	58.6
LAK cells PMA/ionomycin	39.0	NCI-H292 IL-13	35.6

NK Cells IL-2 rest	60.7	NCI-H292 IFN gamma	28.9
Two Way MLR 3 day	55.1	HPAEC none	18.3
Two Way MLR 5 day	36.6	HPAEC TNF alpha + IL-1 beta	44.8
Two Way MLR 7 day	36.6	Lung fibroblast none	28.3
PBMC rest	22.2	Lung fibroblast TNF alpha + IL-1 beta	20.2
PBMC PWM	62.4	Lung fibroblast IL-4	29.1
PBMC PHA-L	42.9	Lung fibroblast IL-9	50.7
Ramos (B cell) none	43.5	Lung fibroblast IL-13	40.3
Ramos (B cell) ionomycin	46.3	Lung fibroblast IFN gamma	37.4
B lymphocytes PWM	40.9	Dermal fibroblast CCD1070 rest	60.3
B lymphocytes CD40L and IL-4	78.5	Dermal fibroblast CCD1070 TNF alpha	92.7
EOL-1 dbcAMP	34.2	Dermal fibroblast CCD1070 IL-1 beta	22.7
EOL-1 dbcAMP PMA/ionomycin	62.0	Dermal fibroblast IFN gamma	24.0
Dendritic cells none	65.1	Dermal fibroblast IL-4	35.6
Dendritic cells LPS	25.3	Dermal Fibroblasts rest	21.8
Dendritic cells anti-CD40	41.8	Neutrophils TNFa+LPS	1.7
Monocytes rest	100.0	Neutrophils rest	18.3
Monocytes LPS	77.4	Colon	11.2
Macrophages rest	62.4	Lung	17.7
Macrophages LPS	15.9	Thymus	81.8
HUVEC none	20.0	Kidney	18.6
HUVEC starved	30.6		

CNS_neurodegeneration_v1.0 Summary: Ag3639 Results from one experiment with the CG59971-01 gene are not included. The amp plot indicates that there were experimental difficulties with this run.

General_screening_panel_v1.4 Summary: Ag3639 Expression of the CG59971-02 gene is ubiquitous in this panel, with highest expression in a breast cancer cell line (CT=26.6). Overall, expression of this gene appears to be higher in samples derived from cancer cell lines than in normal tissues. This widespread expression suggests that this gene product is involved in cell growth and proliferation. Thus, expression of this gene could be used as a marker to

detect the presence of cancer. Furthermore, therapeutic modulation of the expression or function of this gene may be useful in the treatment of cancer.

In addition, this gene is expressed at much higher levels in fetal lung and liver (CTs=29-30) when compared to expression in the adult counterpart (CTs=33). Thus, expression of this gene may be used to differentiate between the fetal and adult sources of these tissue.

Among tissues with metabolic function, this gene is expressed at moderate to low levels in pituitary, adipose, adrenal gland, pancreas, thyroid, and adult and fetal skeletal muscle, heart, and liver. This widespread expression among these tissues suggests that this gene product may play a role in normal neuroendocrine and metabolic and that dysregulated expression of this gene may contribute to neuroendocrine disorders or metabolic diseases, such as obesity and diabetes.

This gene is also highly expressed in the brain, with highest expression in the cerebellum (CT = 28.5), with moderate expression in other CNS regions as well including, amygdala, hippocampus, cerebral cortex, substantia nigra and thalamus. This gene encodes a leucine-rich repeat protein. Leucine rich repeats (LRR) mediate reversible protein-protein interactions and have diverse cellular functions, including cellular adhesion and signaling. Several of these proteins, such as connectin, slit, chaptin, and Toll have pivotal roles in neuronal development in *Drosophila* and may play significant but distinct roles in neural development and in the adult nervous system of humans (Ref. 1). In *Drosophila*, the LRR region of axon guidance proteins has been shown to be critical for their function (especially in axon this gene shows high expression in the brain, it is an excellent candidate neuronal guidance protein for axons, dendrites and/or growth cones in general. Therefore, therapeutic modulation of the levels of this protein, or possible signaling via this protein, may be of utility in enhancing/directing compensatory synaptogenesis and fiber growth in the CNS in response to neuronal death (stroke, head trauma), axon lesion (spinal cord injury), or neurodegeneration (Alzheimer's, Parkinson's, Huntington's, vascular dementia or any neurodegenerative disease).

References:

1. Batty R., Stevens A., Perry R.L., Jacobs J.R. (2001) Repellent signaling by Slit requires the leucine-rich repeats. *J. Neurosci.* 21: 4290-4298.

Panel 4.1D Summary: Ag3639 The CG59971-01 gene is expressed at high to moderate levels in a wide range of cell types of significance in the immune response in health and disease. Highest expression of the gene is seen in resting monocytes (CT=28.6). Significant levels of expression are also seen in members of the T-cell, B-cell, endothelial cell, macrophage/monocyte, and peripheral blood mononuclear cell family, as well as epithelial and fibroblast cell types from lung and skin, and normal tissues represented by colon, lung, thymus and kidney. This ubiquitous pattern of expression suggests that this gene product may be involved in homeostatic processes for these and other cell types and tissues. This pattern is in agreement with the expression profile in General_screening_panel_v1.4 and also suggests a role for the gene product in cell survival and proliferation. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

Example D. Identification of Single Nucleotide Polymorphisms in NOVX nucleic acid sequences

Variant sequences are also included in this application. A variant sequence can include a single nucleotide polymorphism (SNP). A SNP can, in some instances, be referred to as a "cSNP" to denote that the nucleotide sequence containing the SNP originates as a cDNA. A SNP can arise in several ways. For example, a SNP may be due to a substitution of one nucleotide for another at the polymorphic site. Such a substitution can be either a transition or a transversion. A SNP can also arise from a deletion of a nucleotide or an insertion of a nucleotide, relative to a reference allele. In this case, the polymorphic site is a site at which one allele bears a gap with respect to a particular nucleotide in another allele. SNPs occurring within genes may result in an alteration of the amino acid encoded by the gene at the position of the SNP. Intragenic SNPs may also be silent, when a codon including a SNP encodes the same amino acid as a result of the redundancy of the genetic code. SNPs occurring outside the region of a gene, or in an intron within a gene, do not result in changes in any amino acid sequence of a protein but may result in altered regulation of the expression pattern. Examples include alteration in temporal expression, physiological response regulation, cell type expression regulation, intensity of expression, and stability of transcribed message.

SeqCalling assemblies produced by the exon linking process were selected and extended using the following criteria. Genomic clones having regions with 98% identity to all

or part of the initial or extended sequence were identified by BLASTN searches using the relevant sequence to query human genomic databases. The genomic clones that resulted were selected for further analysis because this identity indicates that these clones contain the genomic locus for these SeqCalling assemblies. These sequences were analyzed for putative coding regions as well as for similarity to the known DNA and protein sequences. Programs used for these analyses include Grail, Genscan, BLAST, HMMER, FASTA, Hybrid and other relevant programs.

Some additional genomic regions may have also been identified because selected SeqCalling assemblies map to those regions. Such SeqCalling sequences may have overlapped with regions defined by homology or exon prediction. They may also be included because the location of the fragment was in the vicinity of genomic regions identified by similarity or exon prediction that had been included in the original predicted sequence. The sequence so identified was manually assembled and then may have been extended using one or more additional sequences taken from CuraGen Corporation's human SeqCalling database. SeqCalling fragments suitable for inclusion were identified by the CuraTools™ program SeqExtend or by identifying SeqCalling fragments mapping to the appropriate regions of the genomic clones analyzed.

The regions defined by the procedures described above were then manually integrated and corrected for apparent inconsistencies that may have arisen, for example, from miscalled bases in the original fragments or from discrepancies between predicted exon junctions, EST locations and regions of sequence similarity, to derive the final sequence disclosed herein. When necessary, the process to identify and analyze SeqCalling assemblies and genomic clones was reiterated to derive the full length sequence (Alderborn et al., Determination of Single Nucleotide Polymorphisms by Real-time Pyrophosphate DNA Sequencing. Genome Research. 10 (8) 1249-1265, 2000).

Variants are reported individually but any combination of all or a select subset of variants are also included as contemplated NOVX embodiments of the invention.

NOV5a has one SNP variant, whose variant positions for its nucleotide and amino acid sequences is numbered according to SEQ ID NOs:13 and 14 , respectively. The nucleotide sequence of the NOV5a variant differs as shown in Table SNP1.

Table SNP1. NOV5a variants.

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13376274	143	A	T	47	Gln	Leu

NOV9a has eight SNP variants, whose variant positions for its nucleotide and amino acid sequences is numbered according to SEQ ID NOs:21 and 22 , respectively. The nucleotide sequence of the NOV9a variant differs as shown in Table SNP2.

Table SNP2. NOV9a variants.

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13376043	230	G	T	72	Glu	End
13376044	341	G	A	109	Gly	Arg
13376045	441	A	C	142	Gln	Pro
13376046	532	C	T	172	His	His
13376050	1680	T	C	555	Leu	Ser
13376049	1762	G	T	582	Leu	Phe
13376048	1818	C	T	601	Ser	Leu
13376047	1900	A	G	628	Thr	Thr

NOV14a has five SNP variants, whose variant positions for its nucleotide and amino acid sequences is numbered according to SEQ ID NOs:43 and 44 , respectively. The nucleotide sequence of the NOV14a variant differs as shown in Table SNP3.

Table SNP3. NOV14a variants.

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13376438	1307	T	C	431	Val	Ala
13376437	1571	A	G	519	His	Arg
13376436	1625	T	C	537	Val	Ala
13376435	1646	T	C	544	Val	Ala
13376434	1667	T	C	551	Ile	Thr

NOV15a has twelve SNP variants, whose variant positions for its nucleotide and amino acid sequences is numbered according to SEQ ID NOs:53 and 54 , respectively. The nucleotide sequence of the NOV15a variant differs as shown in Table SNP4.

Table SNP4. NOV15a variants.

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13376083	154	A	G	45	Pro	Pro
13376082	194	T	C	59	Ser	Pro
13376081	253	G	A	78	Arg	Arg
13376080	280	G	A	87	Gln	Gln
13376079	327	C	T	103	Ala	Val
13376078	338	C	T	107	Pro	Ser
13376077	366	T	C	116	Ile	Thr
13376076	502	A	G	161	Lys	Lys
13376069	1069	A	G	350	Pro	Pro
13376072	1137	A	G	373	Gln	Gly
13376071	1264	T	C	415	Leu	Leu
13376070	1367	T	C	450	Ser	Pro

NOV17a has four SNP variants, whose variant positions for its nucleotide and amino acid sequences is numbered according to SEQ ID NOs:61 and 62 , respectively. The nucleotide sequence of the NOV17a variant differs as shown in Table SNP5.

Table SNP5. NOV17a variants.

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13377433	175	T	C	55	His	His
13377432	223	C	G	71	Pro	Pro
13377431	538	G	A	176	Thr	Thr
13377430	680	T	C	224	Phe	Leu

NOV19a has one SNP variant, whose variant positions for its nucleotide and amino acid sequences is numbered according to SEQ ID NOs:71 and 72 , respectively. The nucleotide sequence of the NOV19a variant differs as shown in Table SNP6.

Table SNP6. NOV19a variants.

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13377434	1777	T	A	586	Thr	Thr

NOV21a has one SNP variant, whose variant positions for its nucleotide and amino acid sequences is numbered according to SEQ ID NOs:75 and 76 , respectively. The nucleotide sequence of the NOV21a variant differs as shown in Table SNP7.

Table SNP7. NOV21a variants.

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13377435	7503	T	A	2482	Ala	Ala

NOV38a has two SNP variants, whose variant positions for its nucleotide and amino acid sequences is numbered according to SEQ ID NOs:123 and 124 , respectively. The nucleotide sequence of the NOV38a variant differs as shown in Table SNP8.

Table SNP8. NOV38a variants.

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13377439	801	G	A	232	Ser	Ser
13377441	1595	C	G	497	Pro	Arg

NOV39a has three SNP variants, whose variant positions for its nucleotide and amino acid sequences is numbered according to SEQ ID NOs:125 and 126 , respectively. The nucleotide sequence of the NOV39a variant differs as shown in Table SNP9.

Table SNP9. NOV39a variants.

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13375670	183	C	G	57	His	Gln
13375669	187	C	T	59	Leu	Phe
13377389	1385	A	G	458	His	Arg

NOV46a has four SNP variants, whose variant positions for its nucleotide and amino acid sequences is numbered according to SEQ ID NOs:143 and 144 , respectively. The nucleotide sequence of the NOV46a variant differs as shown in Table SNP10.

Table SNP10. NOV46a variants.

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified

13377442	177	T	C	27	Val	Ala
13377443	590	A	G	165	Thr	Ala
13377444	799	A	G	234	Gln	Gln
13377445	977	T	C	294	Tyr	His

NOV49a has two SNP variants, whose variant positions for its nucleotide and amino acid sequences is numbered according to SEQ ID NOs:151 and 152 , respectively. The nucleotide sequence of the NOV49a variant differs as shown in Table SNP11.

Table SNP11. NOV49a variants.

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13377450	119	A	G	7	Arg	Gly
13377448	1556	G	A	486	Ala	Thr

NOV50a has one SNP variant, whose variant positions for its nucleotide and amino acid sequences is numbered according to SEQ ID NOs:153 and 154 , respectively. The nucleotide sequence of the NOV50a variant differs as shown in Table SNP12.

Table SNP12. NOV50a variants.

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13377451	2371	G	A	791	Ala	Thr

NOV51a has five SNP variants, whose variant positions for its nucleotide and amino acid sequences is numbered according to SEQ ID NOs:155 and 156 , respectively. The nucleotide sequence of the NOV51a variant differs as shown in Table SNP13.

Table SNP13. NOV51a variants.

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13374492	765	G	A	243	Ala	Thr
13374491	924	T	C	296	Phe	Leu
13377453	1028	C	T	330	Pro	Pro
13377454	1052	A	C	338	Ala	Ala
13377455	1205	C	T	389	His	His

NOV52a has one SNP variant, whose variant positions for its nucleotide and amino acid sequences is numbered according to SEQ ID NOs:157 and 158 , respectively. The nucleotide sequence of the NOV52a variant differs as shown in Table SNP14.

Table SNP14. NOV52a variants.

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13377458	221	C	T	37	Arg	Trp

NOV55a has one SNP variant, whose variant positions for its nucleotide and amino acid sequences is numbered according to SEQ ID NOs:163 and 164 , respectively. The nucleotide sequence of the NOV55a variant differs as shown in Table SNP15.

Table SNP15. NOV55a variants.

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13377462	514	C	T	165	Arg	Trp
13377461	993	T	C	324	Ser	Ser

NOV60a has one SNP variant, whose variant positions for its nucleotide and amino acid sequences is numbered according to SEQ ID NOs:183 and 184 , respectively. The nucleotide sequence of the NOV55a variant differs as shown in Table SNP16.

Table SNP16. NOV60a variants.

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13377463	453	T	C	111	Gly	Gly

NOV65a has one SNP variant, whose variant positions for its nucleotide and amino acid sequences is numbered according to SEQ ID NOs:195 and 196, respectively. The nucleotide sequence of the NOV65a variant differs as shown in Table SNP17.

Table SNP17. NOV65a variants.

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13377464	75	C	A	25	Gln	Lys

NOV68a has one SNP variant, whose variant positions for its nucleotide and amino acid sequences is numbered according to SEQ ID NOs:201 and 202, respectively. The nucleotide sequence of the NOV68a variant differs as shown in Table SNP18.

Table SNP18. NOV68a variants.

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13377465	438	C	G	145	Gly	Gly

NOV72a has one SNP variant, whose variant positions for its nucleotide and amino acid sequences is numbered according to SEQ ID NOs:209 and 210, respectively. The nucleotide sequence of the NOV72a variant differs as shown in Table SNP19.

Table SNP19. NOV72a variants.

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13377466	839	C	T	271	Pro	Ser

NOV80a has four SNP variants, whose variant positions for its nucleotide and amino acid sequences is numbered according to SEQ ID NOs:225 and 226, respectively. The nucleotide sequence of the NOV80a variant differs as shown in Table SNP20.

Table SNP20. NOV80a variants.

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13377471	166	G	T	46	Ala	Ser
13377470	482	C	T	151	Ala	Val
13377469	685	A	G	219	Thr	Ala
13377468	1410	G	C	460	Glu	Asp

NOV81a has four SNP variants, whose variant positions for its nucleotide and amino acid sequences is numbered according to SEQ ID NOs:229 and 230, respectively. The nucleotide sequence of the NOV81a variant differs as shown in Table SNP21.

Table SNP21. NOV81a variants.

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13377472	285	C	T	91	His	Tyr
13377473	553	A	G	180	His	Arg
13377474	554	C	T	180	His	His
13377475	2581	A	G	856	Gln	Arg

NOV89a has two SNP variants, whose variant positions for its nucleotide and amino acid sequences is numbered according to SEQ ID NOs:249 and 250, respectively. The nucleotide sequence of the NOV89a variant differs as shown in Table SNP22.

Table SNP22. NOV89a variants.

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13377477	425	A	G	119	Met	Val
13377478	1162	C	A	364	Val	Val

NOV94a has one SNP variants, whose variant positions for its nucleotide and amino acid sequences is numbered according to SEQ ID NOs:269 and 270, respectively. The nucleotide sequence of the NOV94a variant differs as shown in Table SNP23.

Table SNP23. NOV94a variants.

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13377479	1005	T	C	303	Asp	Asp

NOV96a has two SNP variants, whose variant positions for its nucleotide and amino acid sequences is numbered according to SEQ ID NOs:273 and 274, respectively. The nucleotide sequence of the NOV96a variant differs as shown in Table SNP24.

Table SNP24. NOV96a variants.

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13377480	150	A	G	45	Lys	Arg
13377482	2221	A	G	735	Ser	Ser

NOV99a has one SNP variant, whose variant positions for its nucleotide and amino acid sequences is numbered according to SEQ ID NOs:283 and 284, respectively. The nucleotide sequence of the NOV99a variant differs as shown in Table SNP25.

Table SNP25. NOV99a variants.

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13377485	274	T	C	78	Thr	Thr

NOV105a has three SNP variants, whose variant positions for its nucleotide and amino acid sequences is numbered according to SEQ ID NOs:299 and 300, respectively. The nucleotide sequence of the NOV105a variant differs as shown in Table SNP26.

Table SNP26. NOV105a variants.

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13377488	453	C	T	145	Ile	Ile
13377487	828	T	G	270	Thr	Thr
13377486	924	A	G	302	Thr	Thr

NOV113a has three SNP variants, whose variant positions for its nucleotide and amino acid sequences is numbered according to SEQ ID NOs:315 and 316, respectively. The nucleotide sequence of the NOV113a variant differs as shown in Table SNP27.

Table SNP27. NOV113a variants.

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13377490	340	G	A	100	Ala	Thr
13377491	659	C	T	206	Pro	Leu
13377492	726	C	T	228	Arg	Arg
13377493	915	T	C	291	Ala	Ala
13377494	1058	T	C	339	Ile	Thr

13377495	1088	T	C	349	Leu	Pro
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NOV114a has two SNP variants, whose variant positions for its nucleotide and amino acid sequences is numbered according to SEQ ID NOs:319 and 320, respectively. The nucleotide sequence of the NOV114a variant differs as shown in Table SNP28.

Table SNP28. NOV114a variants.

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13375633	185	T	C	54	Val	Ala
13375632	689	A	G	222	Gln	Arg

NOV116a has two SNP variants, whose variant positions for its nucleotide and amino acid sequences is numbered according to SEQ ID NOs:325 and 326, respectively. The nucleotide sequence of the NOV116a variant differs as shown in Table SNP29.

Table SNP29. NOV116a variants.

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13374815	203	A	G	63	Thr	Ala
13374814	384	T	C	123	Leu	Pro

NOV117a has three SNP variants, whose variant positions for its nucleotide and amino acid sequences is numbered according to SEQ ID NOs:329 and 330, respectively. The nucleotide sequence of the NOV117a variant differs as shown in Table SNP30.

Table SNP30. NOV117a variants.

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13377507	453	A	G	149	Pro	Pro
13377506	755	A	T	250	Glu	Val
13377505	1128	G	A	374	Lys	Lys

NOV124a has six SNP variants, whose variant positions for its nucleotide and amino acid sequences is numbered according to SEQ ID NOs:343 and 344, respectively. The nucleotide sequence of the NOV124a variant differs as shown in Table SNP31.

Table SNP31. NOV124a variants.

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13377511	186	C	T	39	Ser	Ser
13377512	372	C	T	101	Gly	Gly
13377513	970	G	T	301	Asp	Tyr
13377514	1051	G	A	328	Val	Met
13377515	1266	C	T	399	Ile	Ile
13377516	1304	A	G	412	Asp	Gly

NOV126a has two SNP variants, whose variant positions for its nucleotide and amino acid sequences is numbered according to SEQ ID NOs:349 and 350, respectively. The nucleotide sequence of the NOV126a variant differs as shown in Table SNP32.

Table SNP32. NOV126a variants.

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13377517	747	T	C	234	Cys	Cys
13377518	1879	C	T	612	Gln	End

OTHER EMBODIMENTS

Although particular embodiments have been disclosed herein in detail, this has been done by way of example for purposes of illustration only, and is not intended to be limiting with respect to the scope of the appended claims, which follow. In particular, it is contemplated by the inventors that various substitutions, alterations, and modifications may be made to the invention without departing from the spirit and scope of the invention as defined by the claims. The choice of nucleic acid starting material, clone of interest, or library type is believed to be a matter of routine for a person of ordinary skill in the art with knowledge of the embodiments described herein. Other aspects, advantages, and modifications considered to be within the scope of the following claims. The claims presented are representative of the inventions disclosed herein. Other, unclaimed inventions are also contemplated. Applicants reserve the right to pursue such inventions in later claims.

What is claimed is:

1. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of:
 - a) a mature form of the amino acid sequence selected from the group consisting of SEQ ID NO: 2n, wherein n is an integer between 1 and 178;
 - b) a variant of a mature form of the amino acid sequence selected from the group consisting of SEQ ID NO: 2n, wherein n is an integer between 1 and 178, wherein any amino acid in the mature form is changed to a different amino acid, provided that no more than 15% of the amino acid residues in the sequence of the mature form are so changed;
 - c) the amino acid sequence selected from the group consisting of SEQ ID NO: 2n, wherein n is an integer between 1 and 178;
 - d) a variant of the amino acid sequence selected from the group consisting of SEQ ID NO: 2n, wherein n is an integer between 1 and 178 wherein any amino acid specified in the chosen sequence is changed to a different amino acid, provided that no more than 15% of the amino acid residues in the sequence are so changed; and
 - e) a fragment of any of a) through d).
2. The polypeptide of claim 1 that is a naturally occurring allelic variant of the sequence selected from the group consisting of SEQ ID NO: 2n, wherein n is an integer between 1 and 178.
3. The polypeptide of claim 2, wherein said allelic variant comprises an amino acid sequence that is the translation of a nucleic acid sequence differing by a single nucleotide from a nucleic acid sequence selected from the group consisting of SEQ ID NO: 2n, wherein n is an integer between 1 and 178.
4. The polypeptide of claim 1 that is a variant polypeptide described therein, wherein any amino acid specified in the chosen sequence is changed to provide a conservative substitution.
5. A method for determining the presence or amount of the polypeptide of claim 1 in a sample, the method comprising:

- (a) providing said sample;
- (b) introducing said sample to an antibody that binds immunospecifically to the polypeptide; and
- (c) determining the presence or amount of antibody bound to said polypeptide, thereby determining the presence or amount of polypeptide in said sample.

6. A method for determining the presence of or predisposition to a disease associated with altered levels of the polypeptide of claim 1 in a first mammalian subject, the method comprising:

- a) measuring the level of expression of the polypeptide in a sample from the first mammalian subject; and
- b) comparing the amount of said polypeptide in the sample of step (a) to the amount of the polypeptide present in a control sample from a second mammalian subject known not to have, or not to be predisposed to, said disease,

wherein an alteration in the expression level of the polypeptide in the first subject as compared to the control sample indicates the presence of or predisposition to said disease.

7. A method of identifying an agent that binds to the polypeptide of claim 1, the method comprising:

- (a) introducing said polypeptide to said agent; and
- (b) determining whether said agent binds to said polypeptide.

8. The method of claim 7 wherein the agent is a cellular receptor or a downstream effector.

9. A method for identifying a potential therapeutic agent for use in treatment of a pathology, wherein the pathology is related to aberrant expression or aberrant physiological interactions of the polypeptide of claim 1, the method comprising:

- (a) providing a cell expressing the polypeptide of claim 1 and having a property or function ascribable to the polypeptide;
- (b) contacting the cell with a composition comprising a candidate substance; and

- (c) determining whether the substance alters the property or function ascribable to the polypeptide;

whereby, if an alteration observed in the presence of the substance is not observed when the cell is contacted with a composition devoid of the substance, the substance is identified as a potential therapeutic agent.

10. A method for screening for a modulator of activity or of latency or predisposition to a pathology associated with the polypeptide of claim 1, said method comprising:

- a) administering a test compound to a test animal at increased risk for a pathology associated with the polypeptide of claim 1, wherein said test animal recombinantly expresses the polypeptide of claim 1;
- b) measuring the activity of said polypeptide in said test animal after administering the compound of step (a); and
- c) comparing the activity of said protein in said test animal with the activity of said polypeptide in a control animal not administered said polypeptide, wherein a change in the activity of said polypeptide in said test animal relative to said control animal indicates the test compound is a modulator of latency of, or predisposition to, a pathology associated with the polypeptide of claim 1.

11. The method of claim 10, wherein said test animal is a recombinant test animal that expresses a test protein transgene or expresses said transgene under the control of a promoter at an increased level relative to a wild-type test animal, and wherein said promoter is not the native gene promoter of said transgene.

12. A method for modulating the activity of the polypeptide of claim 1, the method comprising introducing a cell sample expressing the polypeptide of said claim with a compound that binds to said polypeptide in an amount sufficient to modulate the activity of the polypeptide.

13. An isolated nucleic acid molecule comprising a nucleic acid sequence encoding a polypeptide comprising an amino acid sequence selected from the group consisting of:

- a) a mature form of the amino acid sequence given SEQ ID NO: 2n, wherein n is an integer between 1 and 178;

- b) a variant of a mature form of the amino acid sequence selected from the group consisting of SEQ ID NO: 2n, wherein n is an integer between 1 and 178 wherein any amino acid in the mature form of the chosen sequence is changed to a different amino acid, provided that no more than 15% of the amino acid residues in the sequence of the mature form are so changed;
 - c) the amino acid sequence selected from the group consisting of SEQ ID NO: 2n, wherein n is an integer between 1 and 178;
 - d) a variant of the amino acid sequence selected from the group consisting of SEQ ID NO: 2n, wherein n is an integer between 1 and 178, in which any amino acid specified in the chosen sequence is changed to a different amino acid, provided that no more than 15% of the amino acid residues in the sequence are so changed;
 - e) a nucleic acid fragment encoding at least a portion of a polypeptide comprising the amino acid sequence selected from the group consisting of SEQ ID NO: 2n, wherein n is an integer between 1 and 178 or any variant of said polypeptide wherein any amino acid of the chosen sequence is changed to a different amino acid, provided that no more than 10% of the amino acid residues in the sequence are so changed; and
 - f) the complement of any of said nucleic acid molecules.
14. The nucleic acid molecule of claim 13, wherein the nucleic acid molecule comprises the nucleotide sequence of a naturally occurring allelic nucleic acid variant.
15. The nucleic acid molecule of claim 13 that encodes a variant polypeptide, wherein the variant polypeptide has the polypeptide sequence of a naturally occurring polypeptide variant.
16. The nucleic acid molecule of claim 13, wherein the nucleic acid molecule differs by a single nucleotide from a nucleic acid sequence selected from the group consisting of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178.
17. The nucleic acid molecule of claim 13, wherein said nucleic acid molecule comprises a nucleotide sequence selected from the group consisting of
- a) the nucleotide sequence selected from the group consisting of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178;

b) a nucleotide sequence wherein one or more nucleotides in the nucleotide sequence selected from the group consisting of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178 is changed from that selected from the group consisting of the chosen sequence to a different nucleotide provided that no more than 15% of the nucleotides are so changed;

c) a nucleic acid fragment of the sequence selected from the group consisting of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178; and

d) a nucleic acid fragment wherein one or more nucleotides in the nucleotide sequence selected from the group consisting of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178 is changed from that selected from the group consisting of the chosen sequence to a different nucleotide provided that no more than 15% of the nucleotides are so changed.

18. The nucleic acid molecule of claim 13, wherein said nucleic acid molecule hybridizes under stringent conditions to the nucleotide sequence selected from the group consisting of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178, or a complement of said nucleotide sequence.

19. The nucleic acid molecule of claim 13, wherein the sequence is changed such that no more than 15% of the nucleotides in the coding sequence differ from the nucleotide sequence selected from the group consisting of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178 or a fragment thereof.

20. A vector comprising the nucleic acid molecule of claim 19.

21. The vector of claim 20, further comprising a promoter operably linked to said nucleic acid molecule.

22. A cell comprising the vector of claim 20.

23. A method for determining the presence or amount of the nucleic acid molecule of claim 13 in a sample, the method comprising:

- (a) providing said sample;
- (b) introducing said sample to a probe that binds to said nucleic acid molecule; and

(c) determining the presence or amount of said probe bound to said nucleic acid molecule,
thereby determining the presence or amount of the nucleic acid molecule in said sample.

24. The method of claim 23 wherein presence or amount of the nucleic acid molecule is used as a marker for cell or tissue type.

25. The method of claim 24 wherein the cell or tissue type is cancerous.

26. A method for determining the presence of or predisposition to a disease associated with altered levels of the nucleic acid molecule of claim 13 in a first mammalian subject, the method comprising:

- a) measuring the amount of the nucleic acid in a sample from the first mammalian subject; and
 - b) comparing the amount of said nucleic acid in the sample of step (a) to the amount of the nucleic acid present in a control sample from a second mammalian subject known not to have or not be predisposed to, the disease;
- wherein an alteration in the level of the nucleic acid in the first subject as compared to the control sample indicates the presence of or predisposition to the disease.